

FIGURE 1

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer HS-1 CGTGGCCATCCTGGGCAACACCCCTG
G C GG - CT
G
T

HTRHR	CCTGGGCATTGTAGGCAACATCATGGT
HUMRANTES	CATTGGCCTGGTTGGAAACATCCTGGT
HSBLR1A	CCTGGGCCTGATCGGCAACGTCCTGGT
HUMSOMAT	GGTGGGGCTGGTGGCAACGCCCTGGT
RNU02083	AGTGGGCCTCTCGGAAACTTCCTGGT
U00442	GGTGGGCTTAGTGGCAATTCCCTGGT
HUMNMBR	CGTGGGCTTGCTGGCAACATCATGCT
HSHM4	GGTGACCATCATCGGCAACATCCTGGT
RATAADRE01	CTTGCCATCGTGGCAACATCTTGGT
HUMSSTR3X	GGTGGGCCTGCTGGGTAACTCGCTGGT
HUMC5AAR	GGTGGGAGTGCTGGCAATGCCCTGGT
HUMRDC1A	CATCGGCATGATTGCCAACTCCGTGGT
HUMOPIODRE	CGTGGCGGTGCTCGGCAACCTCGTGGT
RATA2BAR	GCTGGCAGTGGCGGGCAACGTGCTGGT

FIGURE 2

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence to Primer HS-2	TTTGCCATCTGCTGGATGCCAAC C C TTT C G G T T
HUMSGIR	TTTGCCCTCTGCTGGTTCCCTCTAAC
HUMBOMB3S	TTTGCCCTCTGCTGGTTGCCAAATCAC
S46950	TTTGCCCTCTGCTGGCTGCCCTACAC
MUSGPCR	TTTGCCCTCGTCTGGTGCCCTCTAAC
S43387	TTTGCCCTTTATGGATGCCCTACAGG
RATNEURA	TTTGCCATCTGCTGGCTGCCCTATCAC
RATA1ARA	TTTGCCCTCAGCTGGCTGCCGCTGCAT
HUMOPIODRE	TTTGCCATCTGCTGGCTGCCCTATCAC
HUMNEKAR	TTTGCCATCTGCTGGCTGCCCTACAC
RATADENREC	TTTGCCTTGTGCTGGCTGCCCTTGTCC
HUMSRI1A	TTTGTCATCTGCTGGATGCCCTTCTAC
S8637154	TTTGTATCTGCTGGCTGCCCTATCAT
RNCGPCR	TTTGCCGCCTGCTGGATGCCCTTAC
HUMSSTR4Z	TTTGTGCTCTGCTGGATGCCCTTCTAC
RATGNRHA	TTTGCACACTGGTCGAAGCCAGACAAA

FIGURE 3

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer 3A

CTGACCGCTCTIACIACTGACCGATAC
 T T GG GT A C
 G

Primer 3B

CTGACCGCTCTIACIACTGACCGATAT
 T T GG GT A C
 G

L11064

CTCACCATGATGAGCGTGGACCGCTAC

L11065

TTGACCATGATGGAGTGTGACCGCTAC

D16349

CTCTGCACCATGAGCGTGGACCGCTAC

X69676

CTGATGCTCGTGAGTATCGACCGCTAC

M35328

CTTACGGCACTGTCAGCTGACAGGTAC

M73482

CTCACTGCCCTCAGCGCCGACAGGTAC

M73481

CTCACGGCGCTCTCGGCAGACAGATAAC

L08893

TTAACAAATTCTCAGCGCTGACAGATAAC

X62933

ATGACCGCCATGCCGCTGACAGGTAC

X62934

ATGACAACGTGGCCTTGACAGATAAC

J05189

ATGACAGCCATTGCAGTGGACAGGTAT

M60786

CTCTGCCTCTCAGTGTGGACAGGTAC

L04672

CTCACCTGCCCTCAGCATTGACCGCTAC

X61496

TTGCTGGCTATCACTGTGGACCGCTAC

X59249

TTGCTGGCCATTGCTGTAGACCGATAAC

L09249

CTCACCTGCCCTCAGCATTGACCGCTAC

P30731

CTGACAGCTATGCAGTGGACCGCCAC

M31210

CTCCTGCCATGCCATTGAGCGCTAT

U03642

CTCACCGGCCTCAGCTTCGACCGCTAC

FIGURE 4

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer 3C	CTCGCCGCTATIAGCATGGACCGITAC G CC G T T
Primer 3D	CTCGCCGCTATIAGCATGGACCGITAT G CC G T T
L32840	ATTACCTGCATGAGTGTGATAGGTAC
X64052	CTCACGTGTCTCAGCATCGATCGCTAC
M90065	CTCACGTGTCTCAGCATCGATCGCTAC
M91464	CTCACGTGTCTCAGCATTGATCGATAAC
M88096	CTGGTAGCCATCTCTGGAGAGATAT
M99418	CTCGTGGCCATAGCCCTGGAGCGATAAC
L04473	CTCGTGGCCATCGCACTGGAGCGGTAC
M73969	CTGGCCTGCATCAGTGTGGACCGTTAC
X65858	TTGGCCTGCATCAGTGTGGACCGTTAC
S46665	CTGGCTACCATTAGTGCCGACCGTTTC
M60626	ATCGCCCTCATTGCTCTGGACCGCTGT

FIGURE 5

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence TTTACCITCTGGICGCCCTACCAACATC
to Primer 6A GT TC T T

L11064	TTCGTGGTGTGCTGGCGCCATCCACATC
L11065	TTCATCATCTGTTGGACCCCCATTACATC
D16349	TTTATCGTCTGCTGGACCCCCATCCACATC
X69676	TTTGTGCTGTGTTGGTGCCTTCCAGATC
M35328	TTTGCCTTCTGCTGGCTCCCCAACCATGTC
M73482	TTCATCTTCTGTTGGTTCCAAACCATC
M73481	TTCGCCCTCTGCTGGCTCCCCAACATGTC
L08893	TTTGCCCTCTGCTGGTTGCCAAATCACCTC
X62933	TTTGCCATCTGCTGGCTGCCCTACCAACCTC
X62934	TTCGCCATCTGCTGGCTGCCCTACCATC
J05189	TTTGCCATCTGCTGGCTGCCCTATCACGTG
M60786	TTCGCCCTGTGCTGGTTCCCTCTTCACTTA
L04672	TTTGTCACTGCTGGCTGCCCTACCAACGTG
X61496	TTTGCCGCCCTGCTGGATGCCCTTACCCCTC
X59249	TTTGCCTTGTGCTGGCTGCCCTTGTCCATC
L09249	TTTGCCATCTGCTGGCTGCCCTACCAACGTG
P30731	TTTGCCCTCTGCTGGTTCCCTCTCAACTGC
M31210	TTCATGCCCTGCTGGGCACCGCTTCACTC
U03642	TTTGCCCTGTGCTGGATGCCCTACCAACCTG

FIGURE 6

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence TTTTCITTGCTGGITTCCCTACCAACATG
to Primer 6C : C C T G C T T

L32840	TTCATCATTGCTGGCTTCCCTTCCATGTT
X64052	TTCTTCTTTCTGGGTTCCCCACCAAATA
M90065	TTCTTCTTTCTGGGTTCCCCACCAAATA
M91464	TTTTCTTTCTGGATTCCCCACCAAATA
M88096	TTCTTCCTGTGCTGGATGCCATCTCAGC
M99418	TTCTTCCTGTGTTGGCTGCCAGTGTACAGC
L04473	TTTTCTGTGTTGGTTGCCAGTTATAGT
M73969	TTCTGCTTGCTGGCTGCCCTACAAACCTG
X65858	TTCTGCTTGCTGGCTGCCCTACAAACCTG
S46665	TTCTTATCTGGCTGCCCTATCAGGTG
M60626	TTTTCTGTGGTCCCCATATCAGGTG

FIGURE 7

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer T2A

GTCACCAACITGTTCATCCTCAICCTG
 C AC GT T
 : : A

HUMGALAREC	ACCACCAACCTGTTCATCCTCAACCTG
RATADRA1B	CCCACCAACTACTTTATCGTCAACCTG
HUMADRB1	ACCACCAACCTGTTCATCCTCAACCTG
RABIL8RSB	GTCACCGACGTCTACCTGCTGAACCTG
HUMOPIODRE	GTCACCAACTCCTCCTCGTGAACCTG
BTSKR	GTGACCAACTACTTCATCGTCAACCTG
HUMSRI2A	ATCACCAACATTTACATCCTCAACCTG
HUMSSTR3Y	GTCACCAACGTCTACATCCTCAACCTG
HUMGARE	GTCACCAACGCCCTCCTCCTCTCACTG
HUMCCKAR	GTCACCAACATCTCCTCCTCTCCCTG
HUMSHTR	CCCTCCAACCTACCTGATCGTGTCCCTG
HUMD1B	ATGACCAACGTCTTCATCGTGTCTCTG
HUM5HT1E	CCTGCCAACTACCTAATCTGTTCTCTG
HUMD4C	CCCACCAACTCCTCATTGAGCCTG
MMSERO	GCCACCAACTATTCCTGATGTCACTT
RATADRA1A	GTCACCAACTATTCATCGTGAACCTG
S57565	CTGACCAATTGCTTCATTGTGTCCCTG

FIGURE 8

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence AACCCCITCITCTATTGCTTTITCICT
to Primer T7A T T C C C G G

HUMGALAREC	AATCCTATCATTTATGCATTCTCTCT
RATA1ADREC	AACCCCATCGTCTATGCCTTCCGGATC
PIGA2R	AATCCTCTCTTTATGGCTTCTGGGG
RAT5HTRTC	AACCCTATCATCTACCGCTCTTATG
S58541	AACCCCATCATTTATGCCTTAATGCT
HUMGRPR	AACCCCTTGCCCTTACCTGCTGAGC
MUSGRPBM	AACCCCTTGCTCTTATCTGCTGAGC
RRVT1AIIR	AACCCTCTGTTCTACGGCTTCTGGGG
HUMADRB1	AACCCCATCATCTACTGCCGAGCCCC
HSHM4	AACCCCGTGTGCTATGCTCTGTGCAAC
HUMGARE	AACCCCTGGTCTACTGCTTCATGCAC
RATCCKAR	AACCCCATCATCTATTGCTTCATGAAC
S59749	AATCCCAGCTCTACACCTCGCTGGC
HUMSST28A	AACCCCGTCCTCTACGGCTTCCTCTCG
RNGPROCR	AACCCCATCCTCTACGGCTTCCTCTCC
MUSSSRI1A	AACCCCATACTCTACGGCTTCCTGTG
HUMA1AADR	AACCCGCTCATCTACCCCTGTTCCAGC
S66181	AACCCGGTTCTACGCCTTCCTGGAC
HUMSSTR3Y	AACCCCATCCTTATGGCTTCCTCTCC

FIGURE 9

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM1-A2

TGITGGTTATIGGIGTTGTIGGIAA
CC GC C G

MUSBB2R	TGGTGGTGGTGGTGGTGGTGGGCAA
BTSKR	TGGTGCTGGTGGCTGTGATGGGCAA
BOVEETBR	TGTTCGTGCTGGGCATCATCGGAAA
HUMNEYREC	TGATCATTCTTGGTGTCTCTGGAAA
MMSUBKREC	TGGTGCTGGTGGCTGTAACAGGGCAA
HUMPGE2R	TGTTCATCTTCGGGGTGGTGGGCAA
HUMPIR	TGTTCGTGGCCGGTGTGGTGGGCAA
HSU11053	TGTTCGTCGTGGGCTTGGTGGGCAA
RRMC3RA	TGGTGATCCTGGCTGTGGTGGAGGAA
HUMMR	TGGTTATCCTGGCCGTGGTCAGGAA
MUSGRPBM	TCATCGTGTAGGTCTTATTGGCAA
RATCHOLREC	TCTTTCTGATGAGTGTGGCGGAAA
RATCCKAR	TATTCCCTCTCAGTGTGCGGGGAA

FIGURE 10

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence GCCATIACCITGGACAGATACCGAT
to Primer TM3-B2 A T A C G A G

HUMCCKR	GCCATCGCACTGGAGCGGTACAG
HUMCCKBGR	GCCATCGCACTGGAGCGGTACAG
MMGMC5R	GCCATTGCGGTGGACAGGTACA
HUMV2R	GCCATGACGCTGGACCGCCACCG
RATNEURA	GCCATTGCAGTGGACAGGTA
DOGGSTRN	GCCATGCCCTGGAGCGATAACAG
RAT5HT5A	GCAATAGCTTGGACCGCTACTGGT
MUSALP2ADA	GCCATTAGTCTGGACCGCTACTGGT
HUMADORA1X	GCAATTGCTGTGGACCGCTACC
HUMOPIODRE	GCCATCGCGGTGGACAGATAACA
MUSGRPBM	GCACTGTCAGCTGACAGGTACAAA
RATCCKAR	GCCATCTCTGGAGAGATATGG
HSTRHREC	GCCTTACCATGAGAGGTACATA

FIGURE 11

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM3-C2

CATGGCCGTGGAGAGITACITGGC
TT C C T A

HUMNK3R	CATTGCGGTGGACAGGTATATGGC
HSMRNAOXY	CATGTCCCTGGACCGCTGCCTGGC
S68242	CATATCGCTGGAGAGATAACGGAGC
CFGPCR4	CATCGCTCTGGACAGGTACTGGC
MMSUBPREC	TGGCCTTTGACAGATAACATGGC
HUMOPIODRE	CATCGCGGTGGACAGATAACATGGC
HUMGALAREC	ATGTCCGTGGACCGCTACGTGGC
HSS31G	CATTGCCCTGGACAGGTACTGGC
HUMARB3A	CCTGGCCGTGGACCGCTACCTGGC
HUMHPR	CATGGCCGTGGAGCGCTGCCTGGC
RATCCKAR	CATCTCTGGAGAGATAATGGCGC

FIGURE 12

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence : TTTGCCITCTGCTGGATCCCCAAC
to Primer TM6-E2 : C G C G T T

HUMNEKAR	TTTGCCATCTGCTGGCTGCCCTAC
HUMSUBPRA	TTCGCCATCTGCTGGCTGCCCTTC
RATSKR	TTTGCCATCTGCTGGCTGCCCTAC
MUSGRPBM	TTTGCCCTCTGCTGGCTCCCCAAC
HUMOPIODRE	TTTGCCATCTGCTGGCTGCCCTA
HUMA2XXX	TTTGCCCTCTGCTGGCTGCCCT
HUMADRBR	TTCACCCCTCTGCTGGCTGCCCTTC
CFGPCR8	TTCGCCCTCTGTGGCTGCCCT
HUMETSR	TTTGCCCTCTGCTGGCTCCCCCT
MMNPY1CDS	TTCGCCGTCTGCTGGCTGCCCT
HSMRNAOXY	TTCATCGTGTGCTGGACGCCCTTC
RATCCKAR	TTCTTCCTGTGCTGGATGCCCATC

FIGURE 13

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM2F18

ARYYTIGCIITIGCNGAY

HUMTSHX	AACCTGGCCTTGCGGAT
HUMNEKAR	AATCTGGCGCTGGCTGAC
HUMFMLP	AACCTGGCCGTGGCTGAC
HUMINTLEU8	AACCTAGCCTGGCCGAC
HUMA1AADR	AACCTGGCCGTGGCCGAC
HUMIL8RA	AACCTGGCCTGGCCGAC
HSDD2	AGCCTCGCAGTGGCCGAC
HUMANTIR	AATTTAGCACTGGCTGAC
HUMSOMAT	AACCTGGCCGTAGCCGAC
HUMEL4REC	AGCTTGGCTGTGGCTGAT
HSTRHREC	AGCCTGGCAGTAGCTGAT
HSU07882	AACCTGGCCTAGCCGAT

(R = A or G, Y = C or T, N = A, C, G or T, and
I = Inosine)

FIGURE 14

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence TTYNYNNTNTGYTGGITICCI
 to Primer TM6R21

HSBAR	TTCACCCCTCTGCTGGCTGCC
HUMNEKAR	TTTGCCATCTGCTGGCTGCC
HUMETN1R	TTTGCTCTTGCTGGTTCCCT
HUMHISH2R	TTCATCATCTGCTGGTTCCC
HUMA1AADR	TTCGTGCTCTGCTGGTTCCCT
HUMIL8RA	TTCCCTGCTTGCTGGCTGCC
HUMNMBR	TTCATCTTCTGTTGGTTCCCT
HUMNKIRX	TTCGCCATCTGCTGGCTGCC
HUMSUBPRA	TTCGCCATCTGCTGGCTGCC
HUM5HT1DA	TTTATCATCTGCTGGCTGCC
HUMPFPR2A	TTCTTCATCTGTTGGTTCCC
HSDD2	TTCATCATCTGCTGGCTGCC
HUMNEYREC	TTTGCAGTCTGCTGGCTCCCT
HUM2XXX	TTTGCCCTCTGCTGGCTGCC
HUMBK2A	TTCATCATCTGCTGGCTGCC
HUMFMLPX	TTCTTCATCTGTTGGTTCCC
HUMSSTR3X	TTCGTGCTCTGCTGGATGCC
HUMCCKR	TTTTTCTGTGTTGGTTGCCA
HSNEURA	TTTGTGGTCTGCTGGCTGCC

(Y = C or T, N = A, C, G or T, and I = Inosine)

FIGURE 15

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer S3A

GCCTGITAIGATGAGTGTGGAIAGIT
C G C T C

HUMGALAREC	CCCTGGCCGCGATGTCCGTGGACCGCT
S70057	GCCTCGTGGCCATCGCACTGGAGCGGT
S67127	ACCTCTGCGCTCTTAGTGTGACAGGT
S44866	GTCTATGTGCTCTGAGTATTGACAGAT
HUMC5AAR	TCCTGGCCACCATCAGCGCCACCGCT
HUMANTIR	TACTCACGTGTCTCAGCATTGATCGAT
HUMBK2A	TCCTGATGCTGGTGAGCATCGACCGCT
HSNEURA	ACGTGGCCAGCCTGAGTGTGGAGCGCT
HUMGRPR	CACTCACGGCGCTCTGGCAGACAGAT
HUMFSRS	GCCTGACAGTCATGAGCGTGGACCGCT
HUMIL8RA	TGTTGGCCTGCATCAGTGTGGACCGTT
HUMNEKAR	CCATGACCGCCATTGCTGCCGACAGGT

FIGURE 16

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence : TGGITICCCTACCACITIATCAICATC
to Primer S6A : T T GG GT

HUMGALAREC	TGGCTGCCGCACCAACATCATCCATCTC
S70057	TGGTTGCCAGTTATAGTGCCAACACG
S67127	TGGTTCCCTCTTCATTAAAGCCGTATA
S44866	TGGCTTCCCCTTCACCTCAGCAGGATT
HUMC5AAR	TGGTTGCCCTACCAAGGTGACGGGGATA
HUMANTIR	TGGATTCCCCACCAAATATTCACTTT
HUMBK2A	TGGCTGCCCTTCCAGATCAGCACCTTC
HSNEURA	TGGACTCCGTTCCCTCTATGACTTCTAC
HUMGRPR	TGGCTCCCCAATCATGTCATCTACCTG
HUMFSRS	TGGCTGCCCTTCTCACCGTCAACATC
HUMIL8RA	TGGCTGCCCTACAAACCTGGTCCTGCTG
HUMNEKAR	TGGCTGCCCTACCAACCTCTACTTCATC

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FIGURE 17

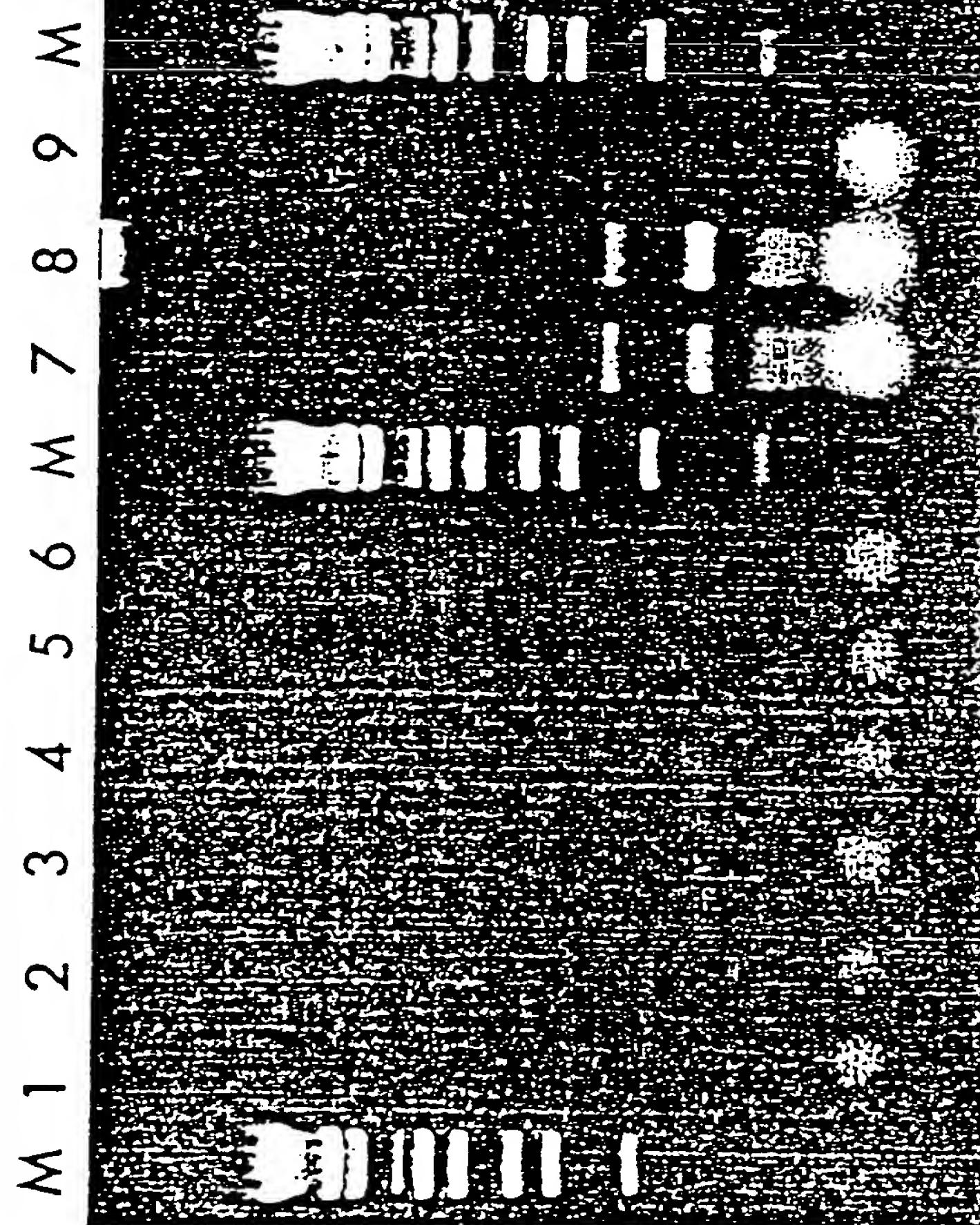


FIGURE 18

FIGURE 19

A58-SP6	10	20	30	40	50
	CAGTGTCCACACCGGGCTGGTCCGCAGTCTTCGTCGTCGACTACACTTCCCT				
HUMSOMATA	X::: :	:::::	:::::	:::::	:::::
	706	716	726	736	746
	60	70	80	90	100
A58-SP6	10	20	30	40	50
	GCTGGGCTTCCTGCTCCGTCGCTGCCATTCGGCTTGCTACCTGCTCA				
HUMSOMATA	::::: :	:::::	:::::	:::::	:::::
	756	766	776	786	796
	110	120	130	140	150
A58-SP6	10	20	30	40	50
	TCGTCGGCAAGATGCGGCCGTCGTCGCCCTGGCGCTGGCAGGCC				
HUMSOMATA	::::: :	:::::	:::::	:::::	:::::
	806	816	826	836	846
	160	170	180	190	200
A58-SP6	10	20	30	40	50
	AGGGCGCTCGGAGAAGAAATCACCGGCTGGTGCTGATGGTCGTGGTGT				
HUMSOMATA	::::: :	:::::	:::::	:::::	:::::
	856	866	876	886	896
	210	220			
A58-SP6	10	20	30	40	50
	<u>CTTGGCCCTCTGCTGGTGTGCCCTCTCCAC</u>				
HUMSOMATA	::::: :	:::::	:::::	:::::	X
	306	916			

FIGURE 20

		10	20	30	40	50
57-A-2		<u>GTGGGCATGCTGGCAACCTCCTGGAAAGGCAGTCGCCGAGGTGGCCGGTT</u>				
HUMDRD5A		X:::	424	434	444	454
		60	70	80	90	100
57-A-2		ACTGGCCCTTGGAGCGTCTGCGACGTCTGGTGGCCTCGACATCATG				
HUMDRD5A		X:::	464	474	484	494
		110	120	130	140	150
57-A-2		TGCTCCACTGCCTCCATCCTGAACCTGTGCGTCATCAGCGTGGACCGCTA				
HUMDRD5A		X:::	514	524	534	544
		160	170	180	190	200
57-A-2		CTGGGCCATCTCCAGGCCCTTCCGCTACAAGCGCAAGATGACTCAGCGCA				
HUMDRD5A		X:::	564	574	584	594
		210	220	230	240	250
57-A-2		TGGCCTTGGTCATGGTCGGCTGGCATGGACCTTGTCCATCCTCATCTCC				
HUMDRD5A		X:::	614	624	634	644
		260	270	280	290	300
57-A-2		TTCATTCCGGTCCAGGTCAACTGGGACAGGGACCAGGCAGGCTTTGGGG				
HUMDRD5A		X:::	664	674	684	694
		310				704
57-A-2		GGGGCTGGACCTGCCAAA				
HUMDRD5A		X:::	714	724		

FIGURE 21

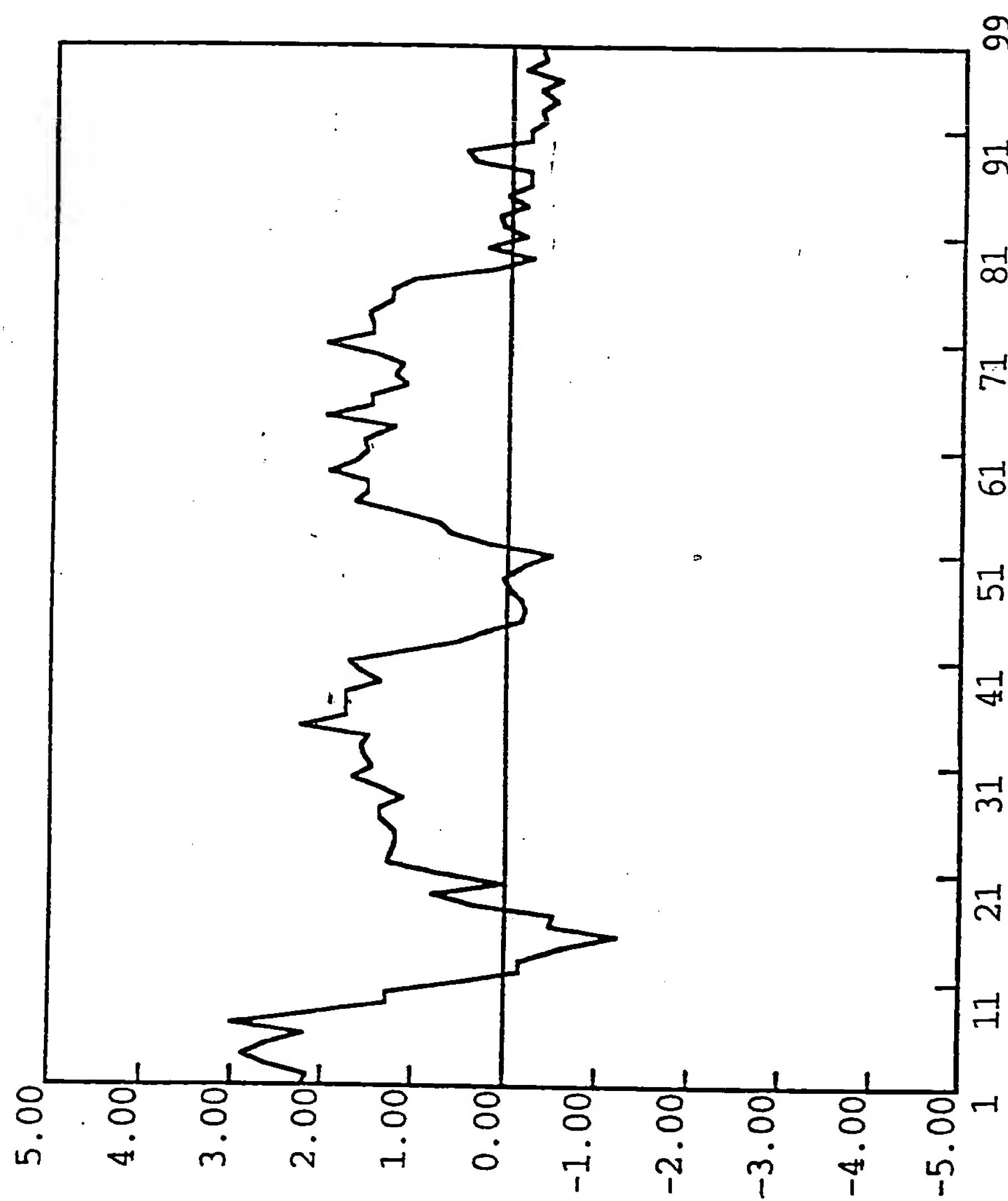
FIGURE 22

FIGURE 23

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FIGURE 24



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FIGURE 25

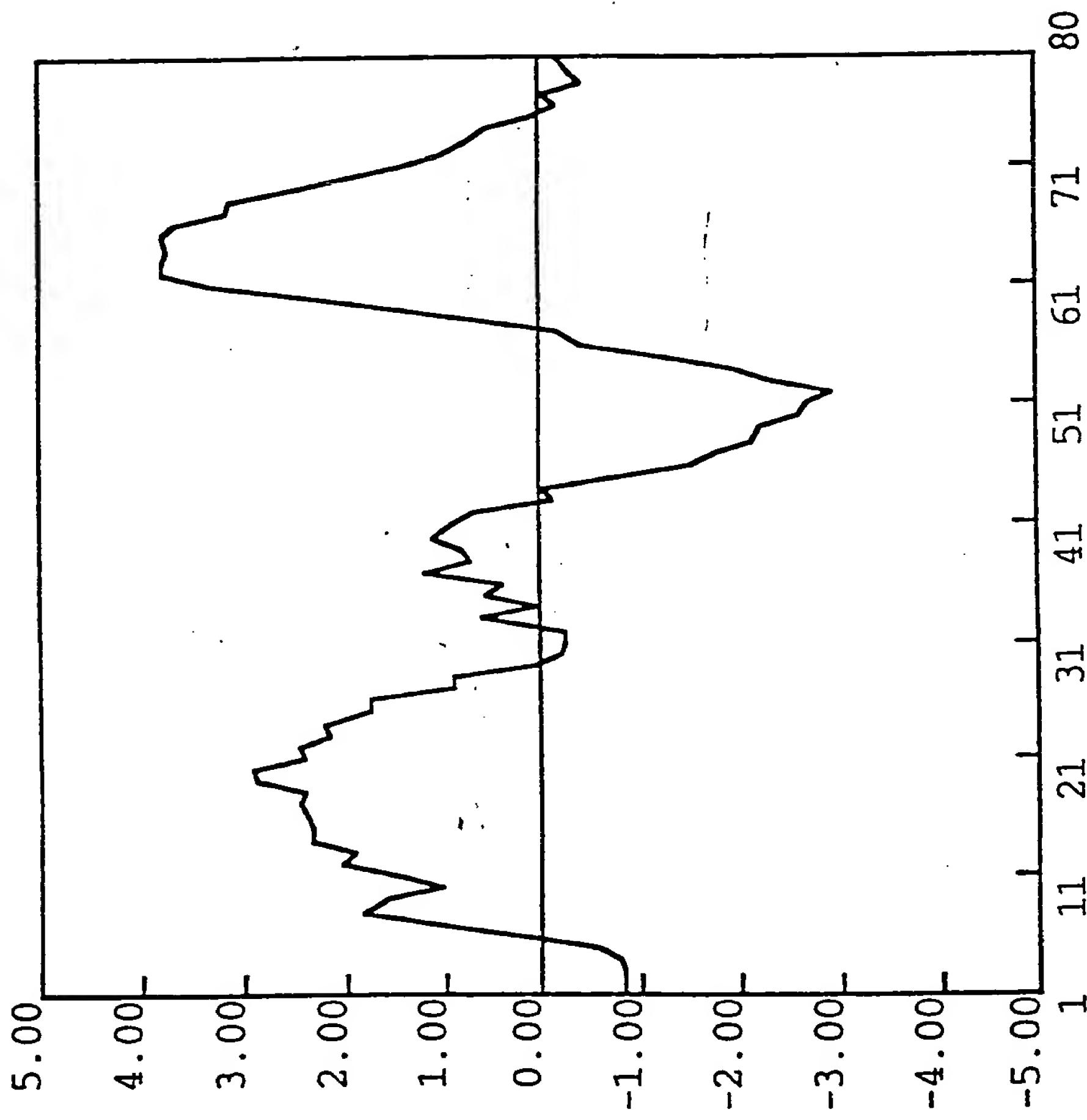


FIGURE 26

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<p>P19P2 1 VGMVGNVLLV LVTARVRRLH NVTNFLIGNL ALSDVLMCTA CVPLTTLAYAF 50</p> <p>S12863 1 LGVSGNLLALI ITLKQKEMR NVTNILIVNL SFSDLVAVM CLPFTFVYTL 50</p>	<p>P19P2 51 EPRGMWVFGGG LCHLVFFLQP VTVYVSVFTL TTIEVDRYVG AGAPAEAGH 100</p> <p>S12863 51 MDH-WVFGET MCKLNPFVQC VSITVSIFSL VLIAVERHQL INPRGWRPN 100</p>	<p>P19P2 101 S12863 101 NRHAYIGITV IWWVLAVASSL PFVIYQILTD EPFQNVSLAA FKDKYVCFDK 150</p>	<p>P19P2 151 S12863 151 FPSDSHRLSY TTLLVQYF GPLCFIFYC VRSVKLRNPV VPVCVTSQA 200</p>	<p>P19P2 201 S12863 201 DWDRARRRT FCLLVVVVV FAICWLPYY 200</p> <p>KYRSSETKRI NVMLLSIVVAA FAVCWLPLT 200</p>	<p>P19P2 210 S12863 210 FCLLVVVVV FAICWLPYY 240</p> <p>230 250</p>
<p>10 20 30 40 50</p>	<p>60 70 80 90 100</p>	<p>110 120 130 140 150</p>	<p>160 170 180 190 200</p>	<p>210 220 230 240 250</p>	

FIGURE 27

9	18	27	36	45	54
5' GTG GGC ATG GTG GGC AAC ATC CTG CTG GTG CTG GTG ATC GCG CGG GTG CGC CGG	---	---	---	---	---
<u>Val Gly Met Val Gly Asn Ile Leu Leu Val Val Ile Ala Arg Val Arg Arg</u>					
63	72	81	90	99	108
CTG TAC AAC GTG ACG AAT TTC CTC ATC GGC AAC CTG GCC TTG TCC GAC GTG CTC	---	---	---	---	---
<u>Leu Tyr Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu</u>					
117	126	135	144	153	162
ATG TGC ACC GCC TGC GTG CCG CTC ACG CTG GCC TAT GCC TTC GAG CCA CGC GGC	---	---	---	---	---
<u>Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly</u>					
171	180	189	198	207	216
TGG GTG TTC GGC GGC CTG TGC CAC CTG GTC TTC CTG CAG GCG GTC ACC	---	---	---	---	---
<u>Trp Val Phe Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr</u>					
225	234	243	252	261	270
GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GCA GTG GAC CGC TAC GTC GTG	---	---	---	---	---
<u>Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val Val</u>					
279	288	297	306	315	324
CTG GTG CAC CCG CTG AGG CGG CGC ATC TCG CTG CGC CTC AGC GCC TAC GCT GTG	---	---	---	---	---
<u>Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val</u>					
333	342	351	360	369	378
CTG GCC ATC TGG GTG CTG TCC GCG GTG CTG GCG CTG CCC GCC GCC GTG CAC ACC	---	---	---	---	---
<u>Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr</u>					
387	396	405	414	423	432
TAT CAC GTG GAG CTC AAG CCG CAC GAC GTG CGC CTC TGC GAG GAG TTC TGG GGC	---	---	---	---	---
<u>Tyr His Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly</u>					
441	450	459	468	477	486
TCC CAG GAG CGC CAG CGC CAG CTC TAC GCC TGG GGG CTG CTG CTG GTC ACC TAC	---	---	---	---	---
<u>Ser Gln Glu Arg Gln Arg Gln Leu Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr</u>					
495	504	513	522	531	540
CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC GCC CGG GTG TCA GTG AAG CTC	---	---	---	---	---
<u>Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu</u>					
549	558	567	576	585	594
CGC AAC CGC GTG GTG CCG GGC CGC GTG ACC CAG AGC CAG GCC GAC TGG GAC CGC	---	---	---	---	---
<u>Arg Asn Arg Val Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg</u>					
603	612	621	630	639	648
GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG GTG GTG GTC GTG GTG GTG TTC ACC	---	---	---	---	---
<u>Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Thr</u>					
657	666				
CTC TGC TGG CTG CCC TTC TTC 3'	---	---	---	---	---
<u>Leu Cys Trp Leu Pro Phe Phe</u>					

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FIGURE 28

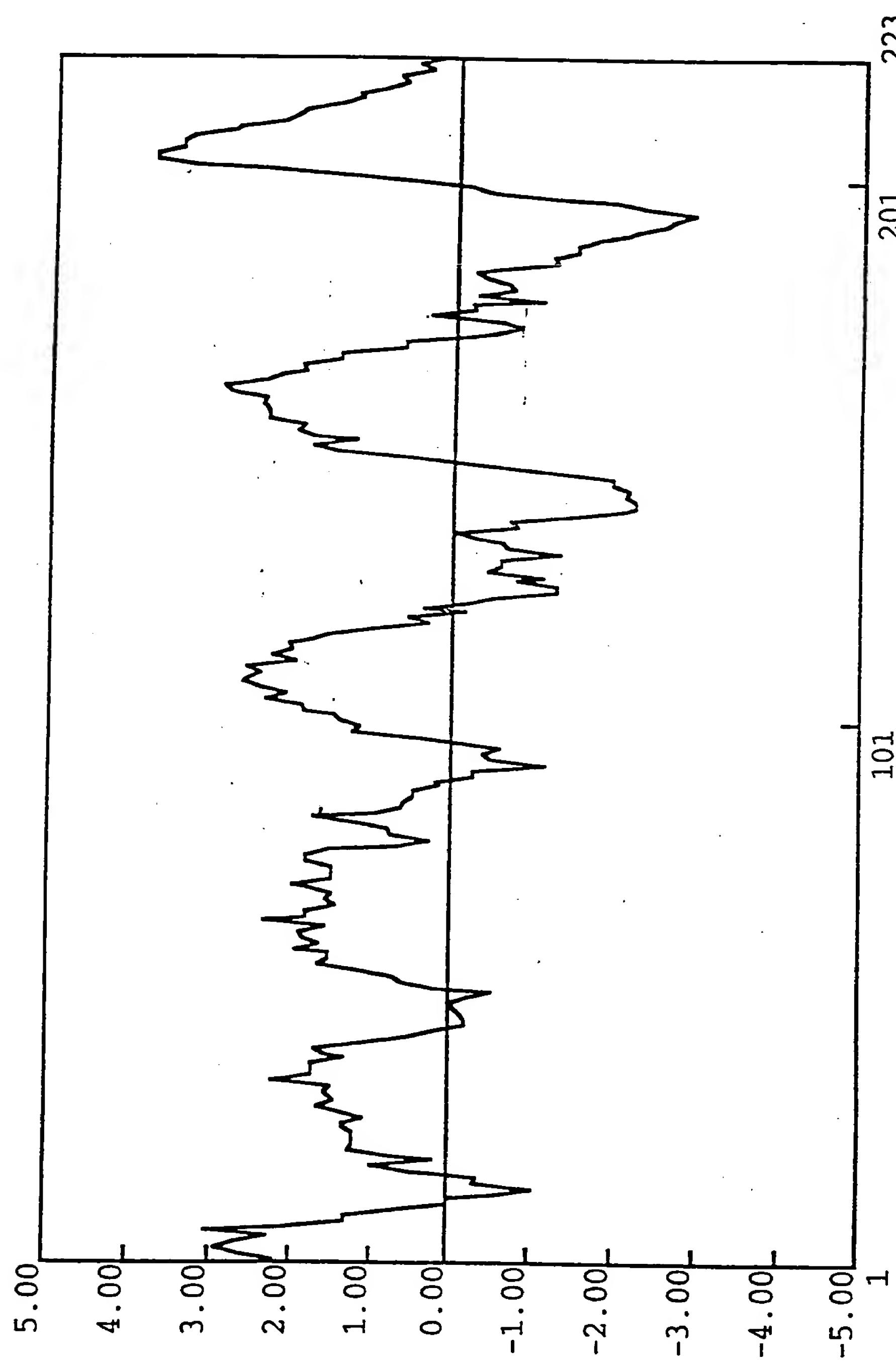


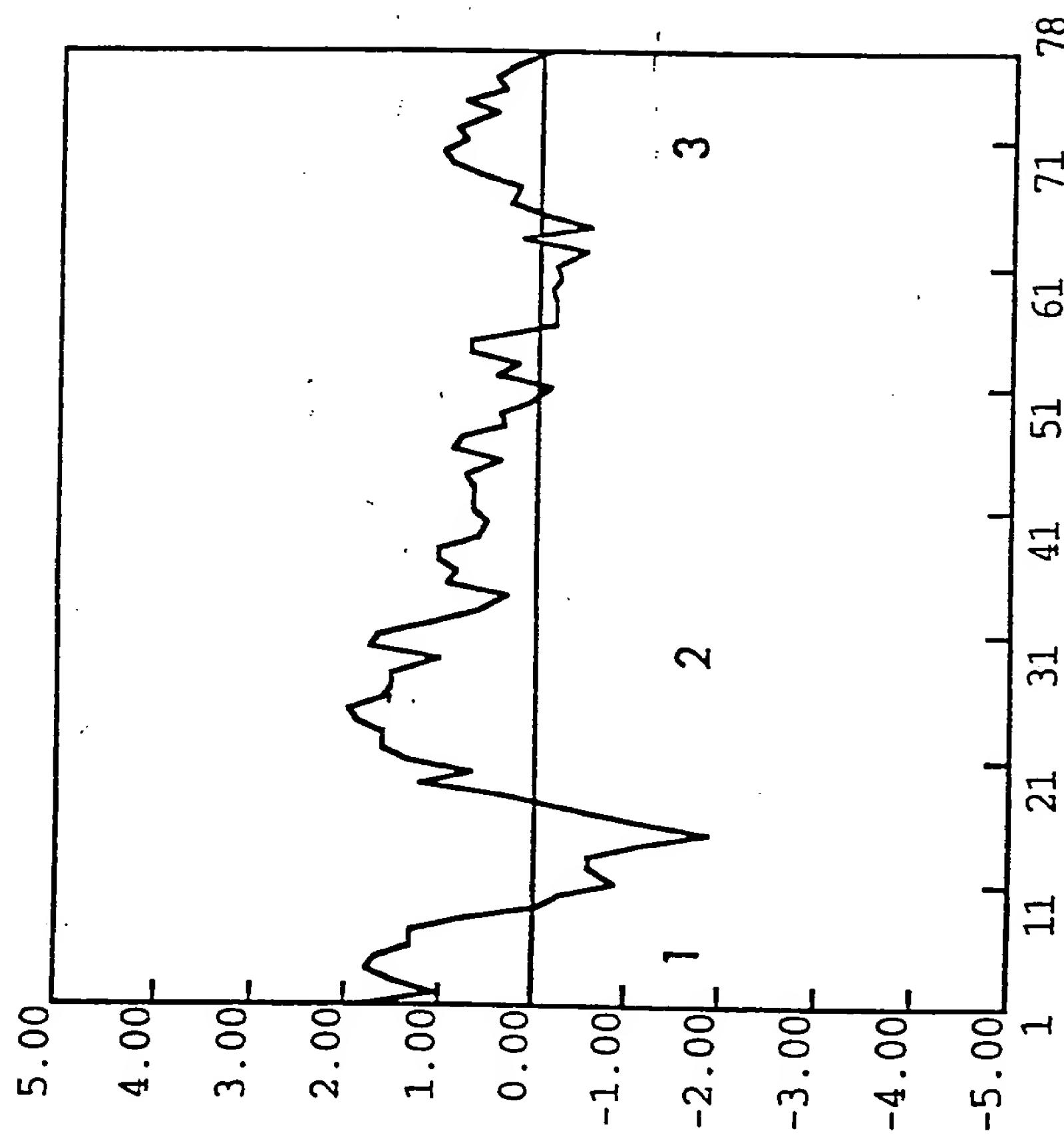
FIGURE 29

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FIGURE 30

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FIGURE 31



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FIGURE 32

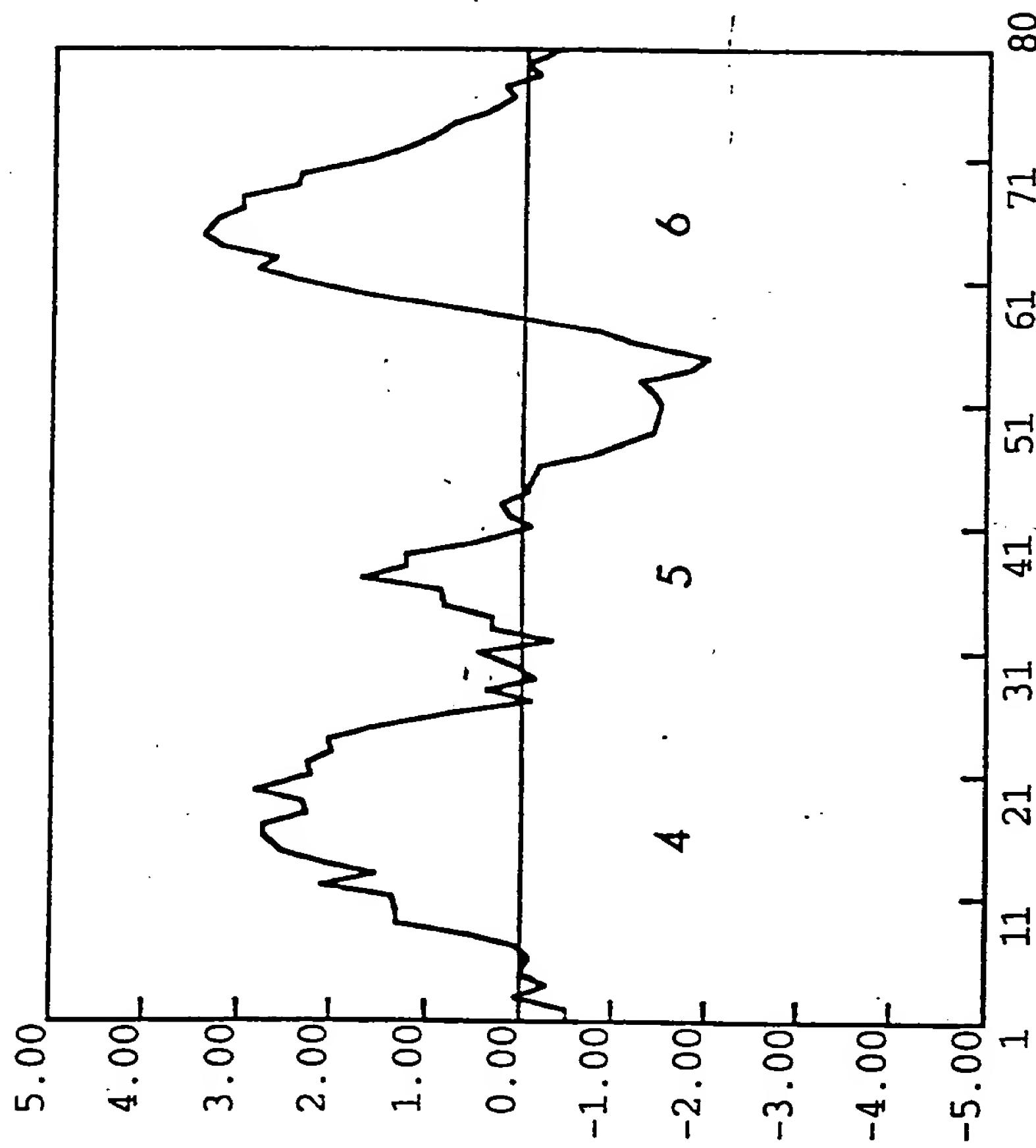


FIGURE 33

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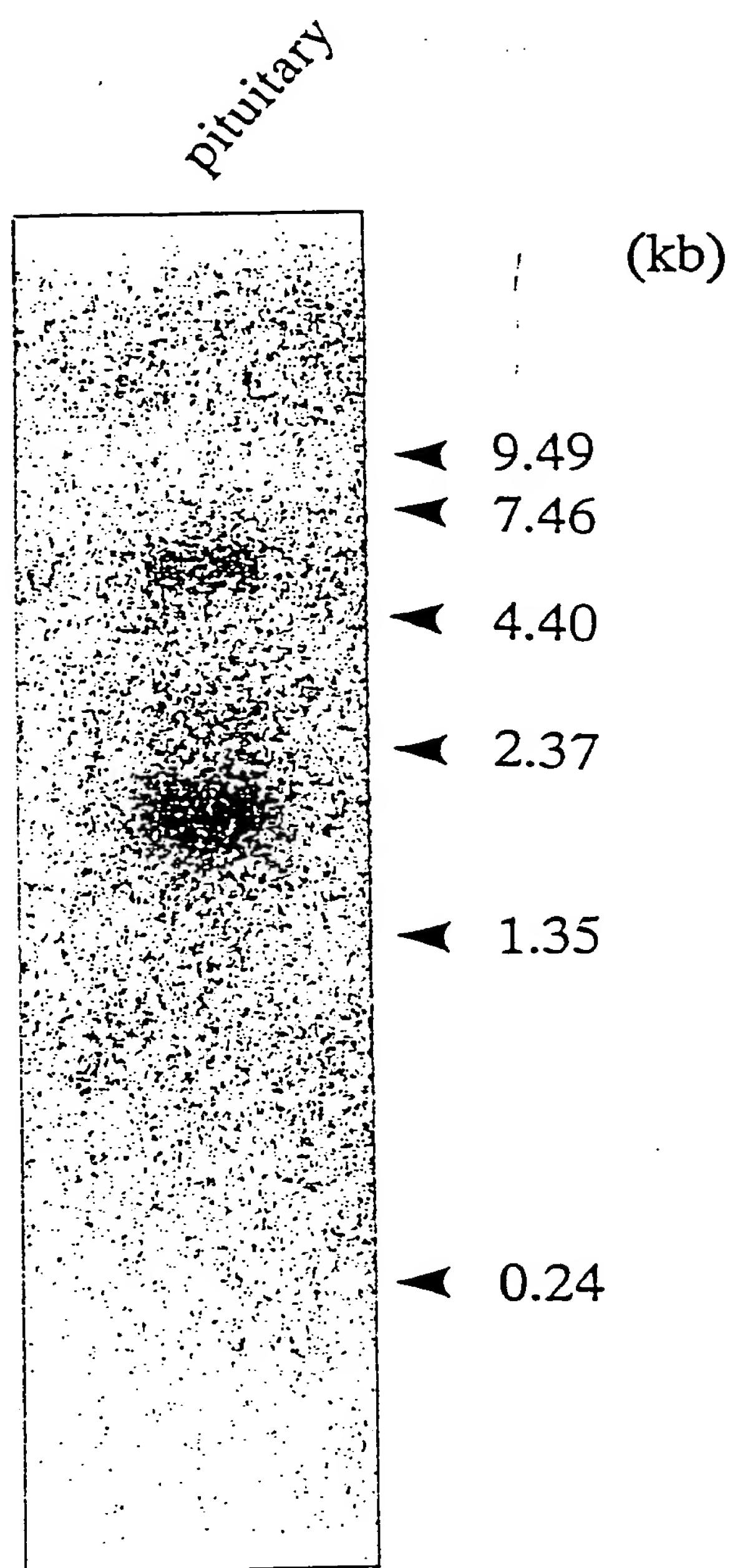
He is the author of the *Principles of the Constitution of the United States*, and of the *Principles of the Constitution of the Commonwealth of Massachusetts*.

FIGURE 34

1	CATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCGAGGGCCAGCAGAAATT	60
1		1
61	CTGCCCTTCTTCCCGCGAGTGCTTCCCGCTCTCCAAACCCACTCCCAGGTGGCCATG	120
1	Met	1
121	GCCTCATCGACCACTCGGGGCCACAGGGTTCTGACTTATTTCTGGGCTGCCGGCG	180
1	AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla	21
181	GTCACAACTCCCGCCAACCAGAGCGCAGAGGCCTCGCGGGCAACGGGTGGTGGCTGGC	240
21	ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly	41
241	GCGGAOGCTCCAGCCGTACGCCCTTCCAGAGCCTGAGCTGGTGCATCAGCTGAAGGGG	300
41	AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly	61
301	CTGATCGTGTGCTCTACAGCGTGTGGTGTGGCTGGTGGGCAACTGCCCTG	360
61	LeuIleValLeuLeuTyrSerValValValValGlyLeuValGlyAsnCysLeuLeu	81
361	GTGCTGGTGATCGCGGGGTGGCGGCCGCTGACAAACGTGACGAACTTCCCTCATCGGCAAC	420
81	ValLeuValIleAlaArgValArgArgLeuHisAsnValThrAsnPheLeuIleGlyAsn	101
421	CTGGCCTTGTCCGACGTGCTCATGTGCACCGCCTGCGTGCCGCTCACGCTGGCTATGCC	480
101	LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla	121
481	TTCGAGCCACGCCGCTGGGTGTTGGCGGGGGCTGTGCCACCTGGCTTCTCCTGCAG	540
121	PheGluProArgGlyTrpValPheGlyGlyLeuCysHisLeuValPhePheLeuGln	141
541	CCGGTCACCGTCTATGTGCGGTGTCACGCTCACCAACCACCGCAGTGGACCGCTACGTC	600
141	ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal	161
601	GTGCTGGTGCACCCGCTGAGCGGGCGCATCTGGCTGGCCCTAGCGCTACGCTGGCTG	660
161	ValLeuValHisProLeuArgArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu	181
561	GCCATCTGGCGCTGTCCGGTGTGGCGCTGCCCGCCGGCTGACACCTATCACGTG	720
181	AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal	201
721	GAGCTCAAGCCGACGACGTGCGCCTCTGCGAGGAGTCTGGGGCTCCCAGGAGGCCAG	780
201	GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln	221
781	CGCCAGCTCTACGCCCTGGGGCTGCTGCTGGCACCTACCTGCTCCCTCTGCTGGTCATC	840
221	ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle	241
841	CCTCTGCTTACGTCCGGTGTCACTGAAGCTCCGCAACCGCGTGGTGCAGGGCTGCGTG	900
241	LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal	261
901	ACCCAGAGCCAGGCCGACTGGGACCGCGCTGGCGCCGGCGACCTCTGCTTGTGGTG	960
261	ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgArgThrPheCysLeuLeuVal	281
961	GTGGTCGTGGTGGTGTTCGCCGTCTGCTGGCTGCCGTGACGTCTCAACCTGCTGGG	1020
281	ValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg	301
1021	GACCTCGACCCCCACGCCATCGACCCCTTACGCCCTTGGCTGGTGCAGCTGCTCTGCCAC	1080
301	AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis	321
1081	TGGCTGCCATGAGTTGGCCTGCTACAACCCCTTCATCTACGCCCTGGCTGCACGACAGC	1140
321	TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer	341
1141	TTCCCGAGGAGCTGCGCAAACCTGGTGGCTGGCCCCGCAAGATAGCCCCCATGGC	1200
341	PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly	361
1201	CAGAATATGACCGTCAGCGGGTCACTGATGCCACTAGCCAGGCCCTGGTCAAGGAGC	1260
361	GlnAsnMetThrValSerValValIle***	371
1261	TCCACTTCAACTGGCCTCTAGGGCACCACTCGAGGTCAATCTGGTGTATTCTCAGCA	1320
371		371
1321	CCAGAGCTAGC	1331
371		371

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FIGURE 35



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FIGURE 36

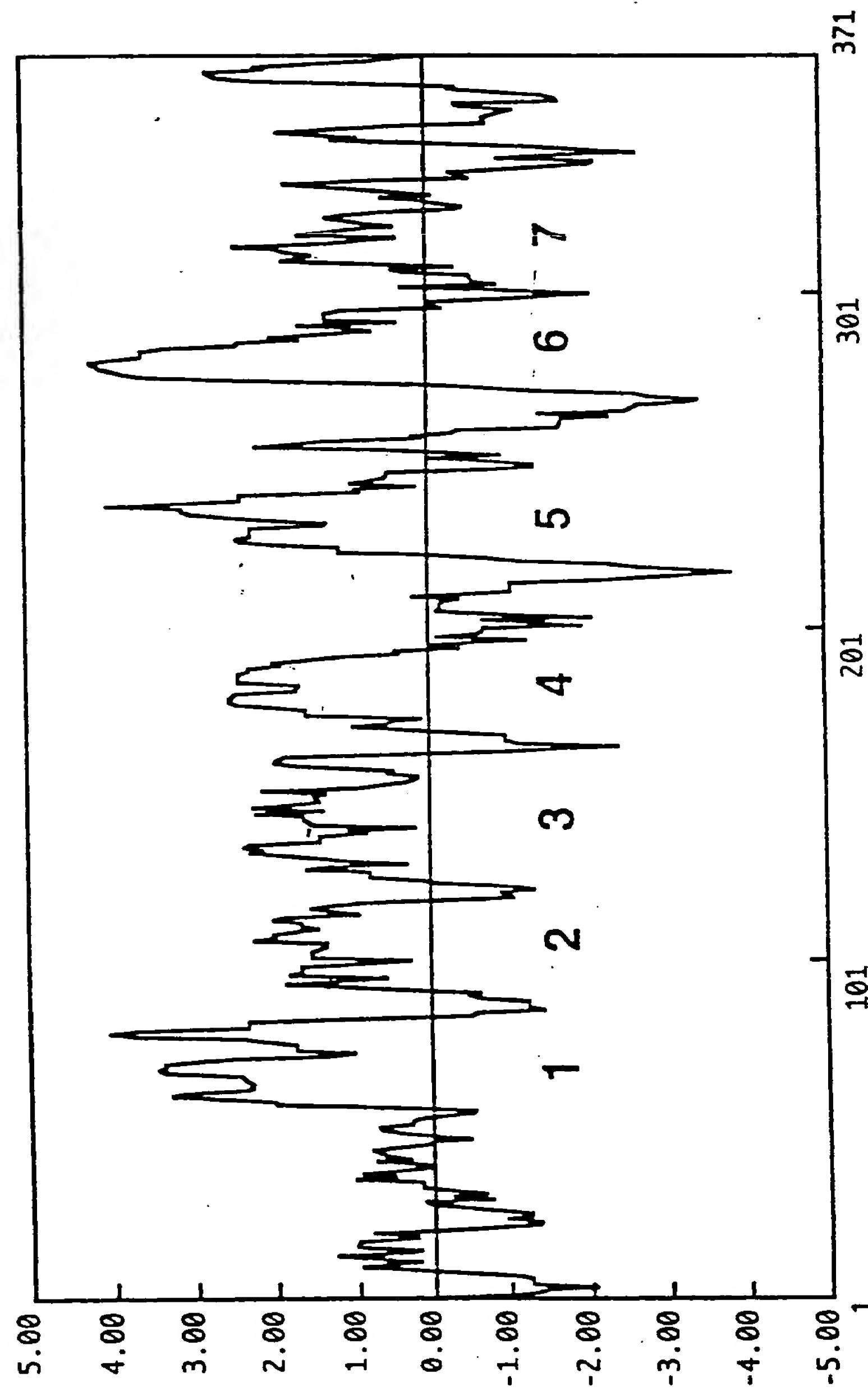


FIGURE 37

5' GTG GGC CTG GTG GGC AAC ATC CTG GCT TCC TGG CAC AAG CGT GGA GGT CGC CGT
 9 18 27 36 45 54
 Val Gly Leu Val Gly Asn Ile Leu Ala Ser Trp His Lys Arg Gly Gly Arg Arg
 GCT GCT TGG GTA GTG TGT GGA GTC GTG TGG CTG GCT GTG ACA GCC CAG TGC CTG
 63 72 81 90 99 108
 Ala Ala Trp Val Val Cys Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu
 CCC ACG GCA GTC TTT GCT GCC ACA GGC ATC CAG CGC AAC CGC ACT GTG TGC TAC
 117 126 135 144 153 162
 Pro Thr Ala Val Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val Cys Tyr
 GAC CTG AGC CCA CCC ATC CTG TCT ACT CGC TAC CTG CCC TAT GGT ATG GCC CTC
 171 180 189 198 207 216
 Asp Leu Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr Gly Met Ala Leu
 ACG GTC ATC GGC TTC TTG CTG CCC TTC ATA GCC TTA CTG GCT TGT TAT TGT CGC
 225 234 243 252 261 270
 Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu Ala Cys Tyr Cys Arg
 ATG GCC CGC CGC CTG TGT CGC CAG GAT GGC CCA GCA GGT CCT GTG GCC CAA GAG
 279 288 297 306 315 324
 Met Ala Arg Arg Leu Cys Arg Gln Asp Gly Pro Ala Gly Pro Val Ala Gln Glu
 CGG CGC AGC AAG GCG GCT CGT ATG GCT GTG GTG GTG GCA GCT GTC TTT GCC CTC
 333 342 351 360 369 378
 Arg Arg Ser Lys Ala Ala Arg Met Ala Val Val Ala Ala Val Phe Ala Leu
 TGC TGG CTG CCT CTC TAC 3'
 387 396
 Cys Trp Leu Pro Leu Tyr

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FIGURE 38

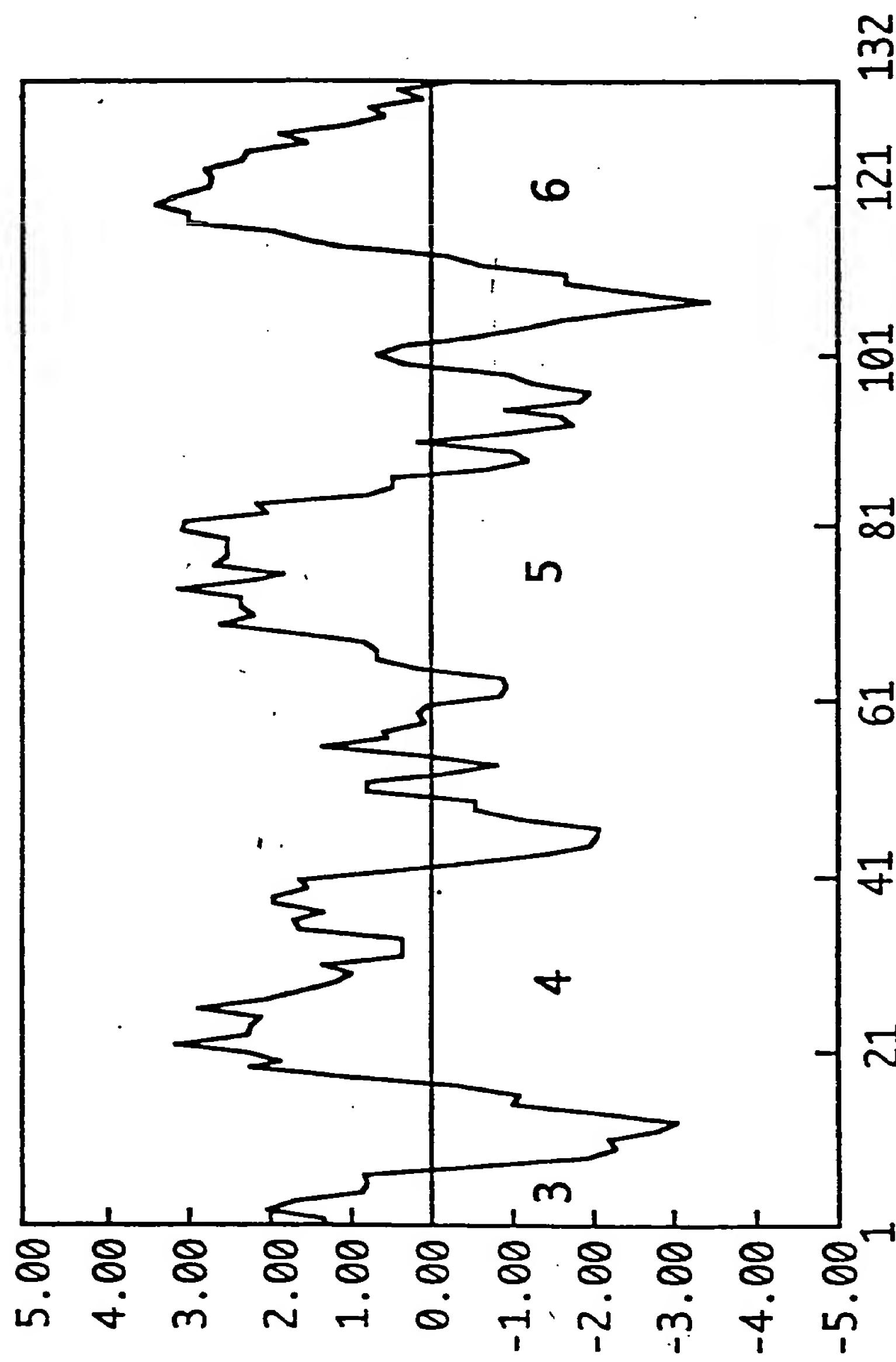


FIGURE 39

P 3H2-17	1	V G L V G N I L A S	W H K R G G R R A A	W V V C G V V W L A	V T A Q C L P T A V	F A A T G I Q R N -	5 0
P 3 4 9 9 6	1	R Y T G V V H P L K	S L G R L K K K N A	V Y V S S L I V W A L	V V A V I A P I L F	Y S G T G V R R N -	5 0
A 4 6 2 2 6	1	R Y L A V V H P T R	S A R W R I T A P V A	R T V S A A V W V A	S A V V V L P V V V	F - - S G V P R G -	5 0
J N 0 6 0 5	1	R Y V A V V H P L R	A A T Y R R P S V A	K L I N L G V W L A	S L L V T L P T A I	F A D T R P A R G G	5 0
S 2 8 7 8 7	1	R Y L A I V H A T N	S O K P R K L I A E	K V V Y V G V W L P	A V L L T I B D L I I	F A D I K E V D E -	5 0
/ 7 9							
P 3H2-17	5 1	R T V - C Y D L - -	S P P I L S T R Y L	P Y G M A L T V I G	F L L P F I A L L A	C Y C R M A R R L C	1 0 0
P 3 4 9 9 6	5 1	K T T T C Y D T - -	T A D E Y L R S Y F	V Y S M C T T V F M	F C I P F I V I L G	C Y G L I V K A L I	1 0 0
A 4 6 2 2 6	5 1	M S T - C H M Q W P	E P A A A W R A G F	I I Y - - T A A L G	F F G P L L V I C I I	C Y L L I V V K V R	1 0 0
J N 0 6 0 5	5 1	Q A V A C N L Q W P	H P A W S A V F V V	Y T F - - - L L G	F L L P V L A I G I I	C Y L L I V G K V R	1 0 0
S 2 8 7 8 7	5 1	R Y I I - C D R F - -	Y P S D L W M L V V E	Q F Q - - H I V V G	L L L P G I V I L S	C Y C I I I S K L S	1 0 0
1 0 0							
P 3H2-17	1 1 0	R Q D G P A - G P V	A Q E - R R S - - K	A A R M A V V V A A	V F A L C W I P L Y	1 5 0
P 3 4 9 9 6	1 0 1	Y K D L D N - S P L	--- R R - - - K	S I Y L V I I V I L T	V F A V S Y L P F H	1 5 0
A 4 6 2 2 6	1 0 1	S A G R R V W A P S	C O R R R R S E R R	V T R M V V A V V A V	L F V L C W M P F Y	1 5 0
J N 0 6 0 5	1 0 1	A V A L R A - - - G	W Q Q R R R S E K K	I T R L V L W V V V	V F V L C W M P F Y	1 5 0
S 2 8 7 8 7	1 0 1	H S K G - - - - -	Y Q K R - - - - - K	A L K T T V I I L	T F F A C W L P Y Y	1 5 0
1 4 0							

FIGURE 40

10 19 28 37 46 55
 5' GTG GGC CTG GTG GGC AAC TTC CTG GCC GCG ATG TCT GTG GAT CGC TAC GTG GCC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Val Gly Leu Val Gly Asn Phe Leu Ala Ala Met Ser Val Asp Arg Tyr Val Ala

 64 73 82 91 100 109
 ATT GTG CAC TCG CGG CGC TCC TCC CTC AGG GTG TCC CGC AAC GCA CTG CTG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Ile Val His Ser Arg Arg Ser Ser Leu Arg Val Ser Arg Asn Ala Leu Leu

 118 127 136 145 154 163
 GCC GTG GGC TTC ATC TCG GCG CTG TCC ATC GCC ATG GCC TCG CCG GTG GCC TAC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Gly Val Gly Phe Ile Trp Ala Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr

 172 181 190 199 208 217
 CAC CAG CGT CTT TTC CAT CGG GAC AGC AAC CAG ACC TTC TGC TGG GAG CAG TGG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 His Gln Arg Leu Phe His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu Gln Trp

 226 235 244 253 262 271
 CCC AAC AAG CTC CAC AAG AAG GCT TAC GTG GTG TGC ACT TTC GTC TTT GGG TAC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Pro Asn Lys Leu His Lys Ala Tyr Val Val Cys Thr Phe Val Phe Gly Tyr

 280 289 298 307 316 325
 CTT CTG CCC TTA CTG CTC ATC TGC TTT TGC TAT GCC AAG GTC CTT AAT CAT CTG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Leu Leu Pro Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val Leu Asn His Leu

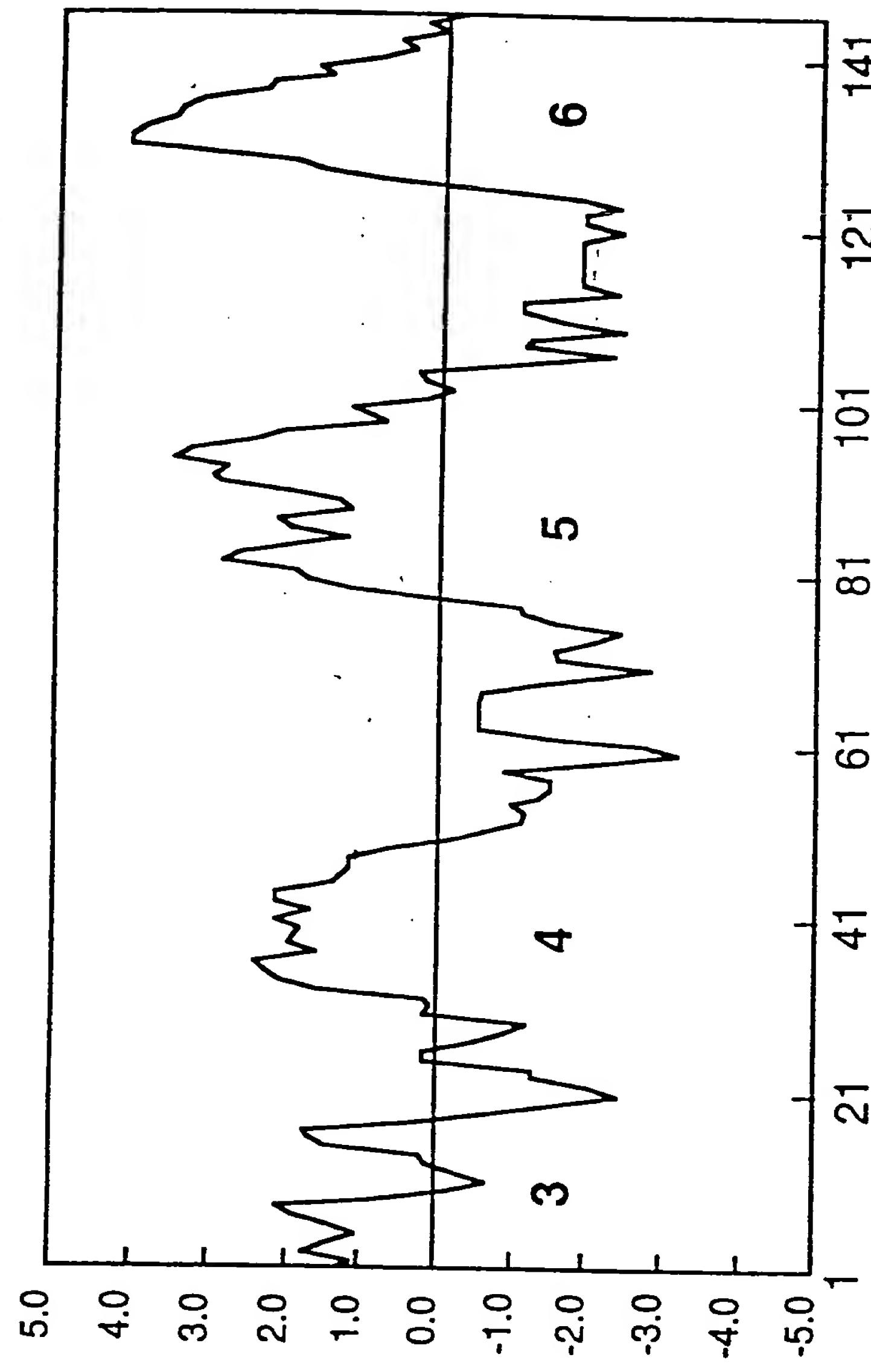
 334 343 352 361 370 379
 CAT AAA AAG CTG AAA AAC ATG TCA AAA AAG TCT GAA GCA TCC AAG AAA AAG ACT
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu Ala Ser Lys Lys Lys Thr

 388 397 406 415 424 433
 GCA CAG ACC GTC CTG GTG GTC GTT GTA TTT GCC CTC TGC TGG CTG CCT TTC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Ala Gln Thr Val Leu Val Val Val Phe Ala Leu Cys Trp Leu Pro Phe

TAC 3'

Tyr

FIGURE 41



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FIGURE 42

p3H2-34 JN0605 B41795 A39297	10	1 VGLVGNF LAA	MSVDRYVAY	ESR RSSSLRV	SRYAL LEVGE	IMASLAMAS	50
	20	1 METSVEGLTV	ESVDRYVAY	HPLRATVYRR	PSVAKLINIG	VMLAISHVYL	50
	30	1 QETSIAGHTV	MSUPRYVAV	HPIKSAKWR	PRDAKMITMA	VMEVSLHVYI	50
	40	1 QETSIIVCUTV	ESVDRYVAVV	HPIKAARYRR	PIVAKVNIG	VWVLSLIVIL	50
	50						
p3H2-34 JN0605 B41795 A39297	60	51 PVA-YHORLF	HRDSNQTF CW	EQWPNKLHK-	-KAYVV-TEV	FGYVLLPLLI	100
	70	51 PTAIEFADTRP	AREGQAVACN	LQWPIBANS-	-AVFVVYTFI	LGFPULLPMLAI	100
	80	51 PIMIYAGLRS	NQWGRSS-CT	TNWFGESGAW	YTGFIIYTFI	LGFPYVPLFI	100
	90	51 PIWVFESRTAA	NSEGIVAA-CN	MLMEPEAQRM	LVGFVLYTFL	MGFULLPMGAI	100
	100						
p3H2-34 JN0605 B41795 A39297	110						
	120						
	130						
	140						
	150						
p3H2-34 JN0605 B41795 A39297	160						
	170						
	180						
	190						
	200						

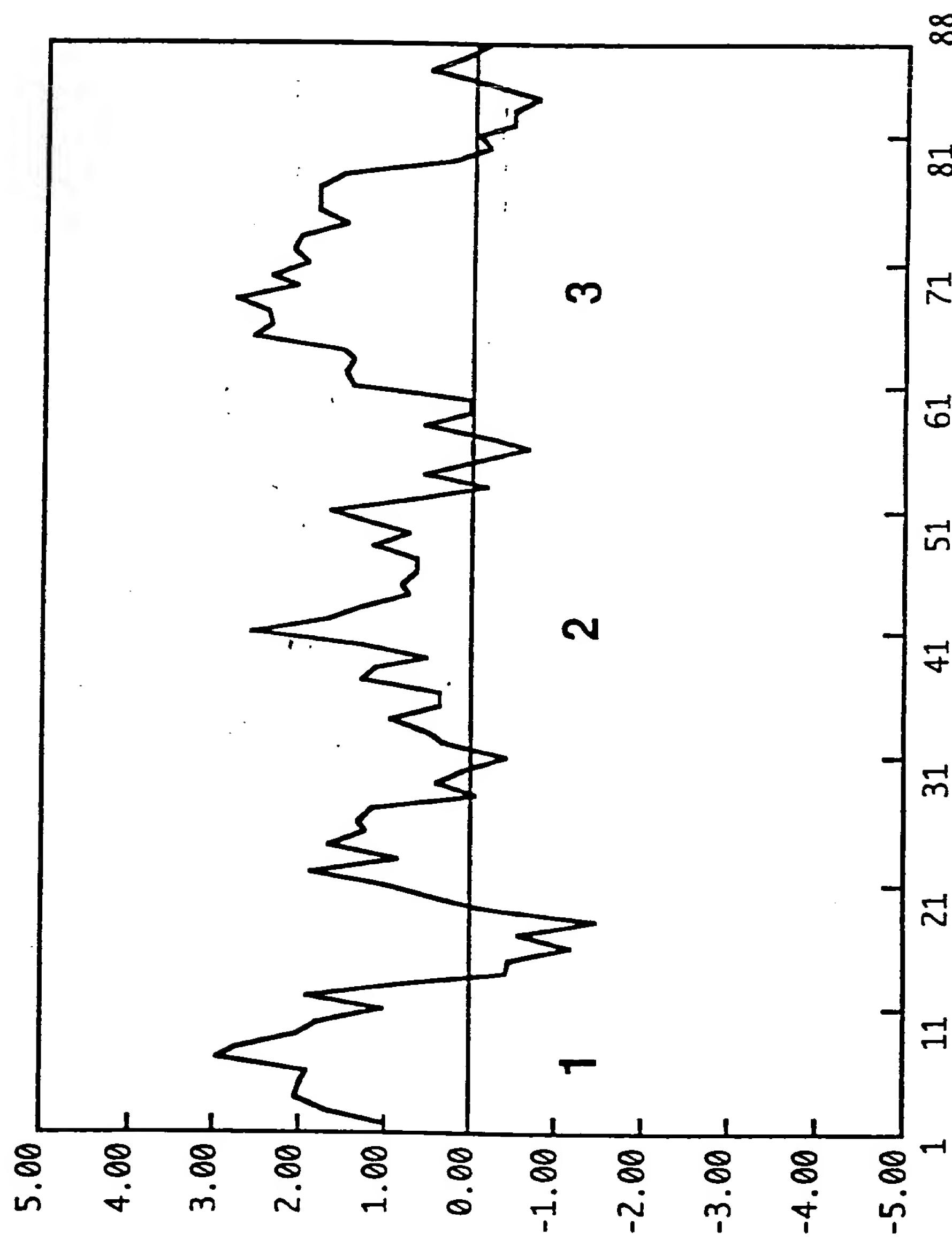
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FIGURE 43

5'	GTG	GCG	ATG	GTG	GGC	AAC	GTC	CTG	GTG	CTG	TTC	TTC	GCC	TTC	TCC	ATC	ATC	MAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Val	Gly	Met	Val	Gly	Asn	Val	Leu	Val	Leu	Trp	Phe	Phe	Gly	Phe	Ser	Ile	Ile	Lys
64	64	73	73	82	82	91	91	100	100	109	109	109	109	109	109	109	109	109
AGG	ACC	CCC	TTC	TCC	GTC	TAC	TTC	CTG	CAC	CTG	GCC	AGC	GCC	GAC	GGC	GCC	GCC	TAC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Arg	Thr	Pro	Phe	Ser	Val	Tyr	Phe	Leu	His	Leu	Ala	Ser	Ala	Asp	Gly	Ala	Tyr	Ala
118	118	127	127	136	136	145	145	154	154	154	154	154	154	154	154	154	154	163
CTC	TTC	AGC	AAG	GCC	GTC	TTC	TCC	CTG	CTG	AAC	GCC	GGC	GGC	TTC	CTG	CTG	GGC	ACC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Leu	Phe	Ser	Lys	Ala	Val	Phe	Ser	Leu	Leu	Asn	Ala	Gly	Gly	Phe	Leu	Gly	Thr	Thr
172	172	181	181	190	190	199	199	208	208	217	217	217	217	217	217	217	217	217
TTC	GCC	CAC	TAT	GTG	CCG	AGC	GTG	GCC	CGG	GTG	CGG	CTG	CTG	TTC	TTC	TTC	TTC	TTC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Phe	Ala	His	Tyr	Val	Arg	Ser	Val	Ala	Arg	Val	Leu	Gly	Leu	Cys	Ala	Phe	Val	Val
226	226	235	235	244	244	253	253	262	262	262	262	262	262	262	262	262	262	262
GCG	GGC	GTG	AGC	CTC	CTG	CCG	GCC	GTG	AGC	ATG	GAG	CGC	TTC	GGG	TCT	G	3'	3'
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Ala	Gly	Val	Ser	Leu	Leu	Pro	Ala	Val	Pro	Ala	Val	Ser	Met	Glu	Arg	Cys	Ala	Ser

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FIGURE 44



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FIGURE 45

FIGURE 46

1	CAAACCAACAGGTGCAACCTCAAGGCACTGAAAGCAGGGACGCAGCTACAAGGCCAAGGGATTGAACC	72
1		1
73	CATAACCGCTCAGAAGATTCTCCGCCTGCGGAGAGCTGCGGAGGAGTCCCACCCGTCCAGCTGCTGACTGC	144
1		1
145	GAGCAGTGAGAGTCGCCTAGACCCGTACCTCTGTGTTCTGGAGCCTGCCGCCCCGGCACGGAAAGGCTTAG	216
1		1
217	CTCGGGACTTGCAGCACCGCCTCCCTCTTACGCCAGGCCAGGAGGATAGTGTGATGGGACAGCCAGG	288
1		1
289	GTCGCTCTCCAGGCTTCTGCGGGTTGCGGGAGGTACTAGTTGGAGACGGCGCGCTCGCTCTGCCGCT	360
1		1
361	CTGTCCCTGGGCCACTCCGTGATCCTAGGCTACCTCCAGAGCCAGTTTCCCTGGCTGGCACAACTCTCCAGG	432
1		1
433	GCGCTCCGGTCCGTTCGACAGGCCCAAGGGGTATCCAGTAAGTGTGAACTGGCTATGGTGAACCTC	504
1	MetGluLeuAlaMetValAsnLeu	8
505	AGTGAAGGGAATGGGAGCGACCCAGAGCCGCCAGCCCCGGAGTCCAGGCCCTTCCGGCATGGCGTGGAG	576
8	SerGluGlyAsnGlySerAspProGluProProAlaProGluSerArgProLeuPheGlyIleGlyValGlu	32
577	AACTTCATTACGCTGGTAGTGTGTTGGCCTGATTTCGCGATGGCGTGCTGGCAACAGCCTGGTGTGATCACC	648
32	AsnPheIleThrLeuValValPheGlyLeuIlePheAlaMetGlyValLeuGlyAsnSerLeuValIleThr	56
649	GTGCTGGCGCGAGCAAACCAAGGCAAGCCGCCAGCACCAACCTGTTATCCTCAATCTGAGCATCGCA	720
56	ValLeuAlaArgSerLysProGlyLysProArgSerThrThrAsnLeuPheIleLeuAsnLeuSerIleAla	80
721	GACCTGGCCTACCTGCTCTTGCATCCCTTTCAGGCCACCGTGTATGCACIGCCCACCTGGGTGCTGGC	792
80	AspLeuAlaTyrLeuLeuPheCysIleProPheGlnAlaThrValTyrAlaLeuProThrTrpValLeuGly	104
793	GCCTTCATCTGCAAGTTTACACTACTCTTCACCGTGTCCATGCTGGTAGCATCTCACCCCTGGCCCG	864
104	AlaPheIleCysLysPheIleHisTyrPhePheThrValSerMetLeuValSerIlePheThrLeuAlaAla	128
865	ATGTCTGTGGATCGTACGTGGCCATTGTGCACTCGCGCGCTCCTCCCTCAGGGTGTCCCAGCAACGCA	936
128	MetSerValAspArgTyrValAlaIleValHisSerArgArgSerSerLeuArgValSerArgAsnAla	152
937	CTGCTGGCGTGGCTTCATCTGGCGCTGTCTCGCCATGGCGTGGCTACCACCGCTGCTTT	1008
152	LeuLeuGlyValGlyPheIleTrpAlaLeuSerIleAlaMetAlaSerProValAlaTyrHisGlnArgLeu	176
1009	TTCCATGGGACAGCAACCAAGACCTCTGCTGGGAGCAGTGGCCAAACAAGCTCCACAAGAAGGCTTACGTG	1080
176	PheHisArgAspSerAsnGlnThrPheCysTrpGluGlnTrpProAsnLysLeuHisLysAlaTyrVal	200
1081	GTGTGCACTTCGTTGGTACCTCTGCCCTACTGCTCATCTGCTTTGCTATGCCAAGGTCTTAAT	1152
200	ValCysThrPheValPheGlyTyrLeuLeuProLeuLeuIleCysPheCysTyrAlaLysValLeuAsn	224
1153	CATCTGCATAAAAAGCTGAAAAAACATGTCAAAAAAAGCTGAAAGCATCCAAGAAAAAGACTGCACAGACCGTC	1224
224	HisLeuHisLysLeuLysAsnMetSerLysSerGluAlaSerLysLysThrAlaGlnThrVal	248
1225	CTGGTGGTGGTGTAGTATTGGCATATCCTGGCTGCCCATCATGTCGTCCACCTCTGGCTGAGTTGGA	1296
248	LeuValValValValPheGlyIleSerTrpLeuProHisHisValValHisLeuTrpAlaGluPheGly	272
1297	GCCTTCCCACGTGCCAGCTTCTCTTCTCAGAAATCACGCCATTGCCATACAGCAACTCCTCA	1368
272	AlaPheProLeuThrProAlaSerPhePhePheArgIleThrAlaHisCysLeuAlaTyrSerAsnSer	296
1369	GTGAACCCCATCATATATGCCCTCTCAGAAAACCTCCGGAGGGTACAAGCAAGTGTCAAGTGTCA	1440
296	ValAsnProIleIleTyrAlaPheLeuSerGluAsnPheArgLysAlaTyrLysGlnValPheLysCysHis	320
1441	GTTTGCATGAACTCCACGGAGTGAACACTAAGGAAACAAAGAGCCGGATGGACACCCGCCATCCACCAAC	1512
320	ValCysAspGluSerProArgSerGluThrLysGluAsnLysSerArgMetAspThrProProSerThrAsn	344
1513	TGCACCCACGTGTGAAGGTTGCGGGAGCCTCCGACTTCCAGCTCCATGTGTTAGAGAGAGGGAGGGCG	1584
344	CysThrHisVal***	349
1585	GAGCGAATTATCAAGTAACATGG	1607
349		349

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FIGURE 47

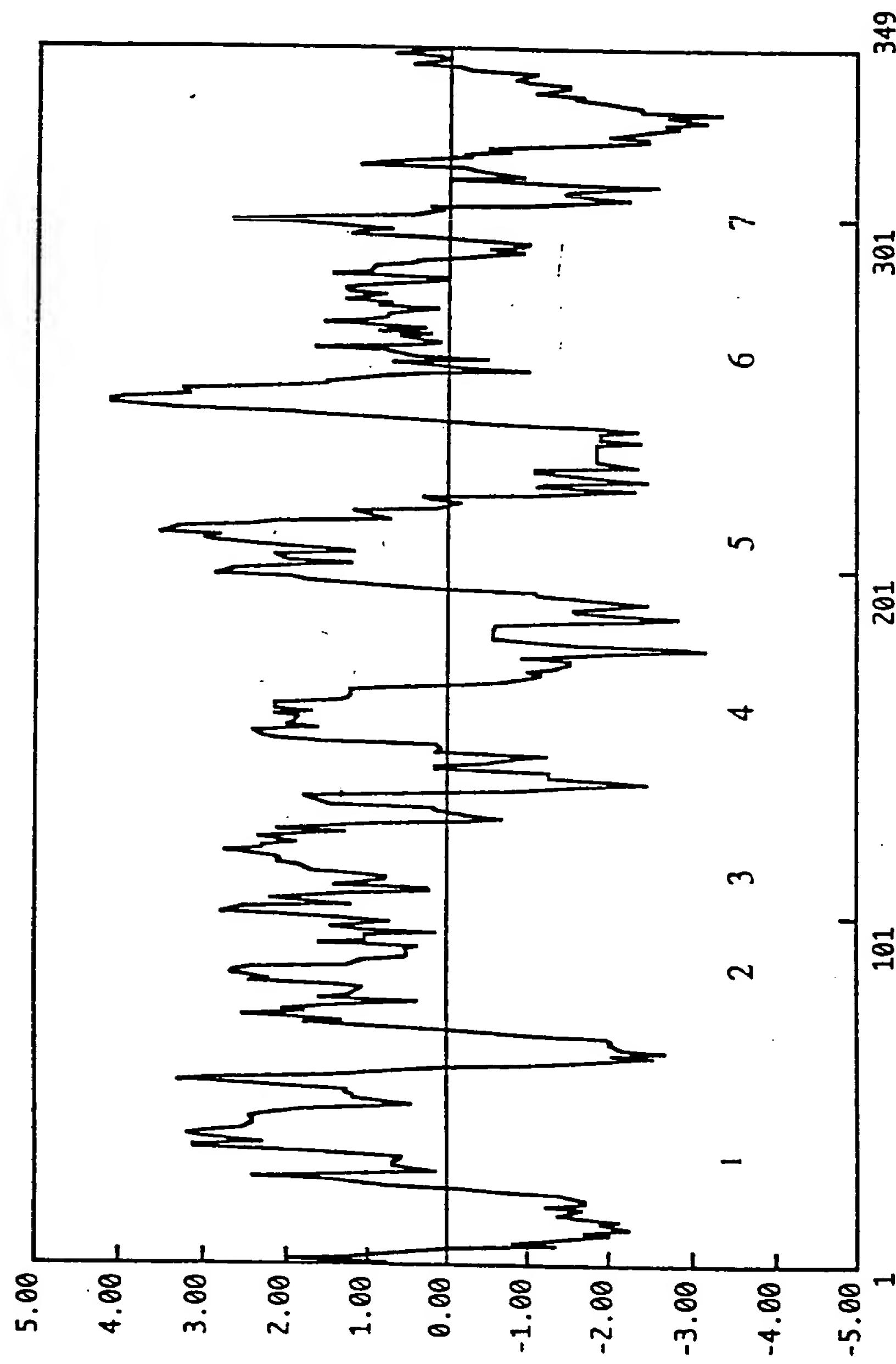


FIGURE 48

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MOUSEGALRECE	1	MELAVNISE	10	GNCSDPPEPPA	20	PFSPRPLFEGIC	30	VENFILTLVVF	40	GHTFAMGVLG	50
HUMGALAMI	1	MELAVNISE	10	GNASCPEPPA	20	PEPGPLFEGIC	30	VENFVTLVVF	40	GLTFALGVLG	50
MOUSEGALRECE	51	NSLUVITVLR	60	SKPGKPRSTT	70	DLAYLLEFCIP	80	FOATVYALIPT	90	FOATVYALIPT	100
HUMGALAMI	51	NSLUVITVLR	60	SKPGKPRSTT	70	DLAYLLEFCIP	80	FOATVYALIPT	90	FOATVYALIPT	100
MOUSEGALRECE	101	WVLGAFICKF	110	IHYEFFTVSMT	120	VSIFTPLAAMS	130	VPRYYATWHS	140	RRSSSLRVSR	150
HUMGALAMI	101	WVLGAFICKF	110	IHYEFFTVSMT	120	VSIFTPLAAMS	130	VDRYVATWHS	140	RRSSSLRVSR	150
MOUSEGALRECE	151	NALLGVGFIW	160	ALSTAMASPV	170	AHQLEH-R	180	DSNQTECWEQ	190	WPVNLHKAY	200
HUMGALAMI	151	NALLGVGFIW	160	ALSTAMASPV	170	AHQLEH-R	180	ASNQTECWEQ	190	WPDPRHKKAY	200
MOUSEGALRECE	201	WVCTFVFGYL	210	LPFLLICFCY	220	AKVLNLHLHKK	230	LNKMSKKSEA	240	SKKTTAQTVL	250
HUMGALAMI	201	WVCTFVFGYL	210	LPFLLICFCY	220	AKVLNLHLHKK	230	LNKMSKKSEA	240	SKKTTAQTVL	250
MOUSEGALRECE	251	WVWVFGISW	260	EFPHHWWLWA	270	EFGAEPLTPA	280	SFFERITAHIC	290	LAYSNSSSVNP	300
HUMGALAMI	251	WVWVFGISW	260	EFPHHWWLWA	270	EFGAEPLTPA	280	SFFERITAHIC	290	LAYSNSSSVNP	300
MOUSEGALRECE	301	WVYVFGISW	310	TKAYKQVFKC	320	TKENKSRIDT	330	PPSTNCTHVK	340	PPSTNCTHVK	350
HUMGALAMI	301	WVYVFGISW	310	TKAYKQVFKC	320	TKENKSRIDT	330	PPSTNCTHVK	340	PPSTNCTHVK	350
MOUSEGALRECE	351	X.....	360	X.....	370	X.....	380	X.....	390	X.....	400
HUMGALAMI	351	X.....	360	X.....	370	X.....	380	X.....	390	X.....	400

FIGURE 49

5. 9 18 27 36 45 54

CTC GCG GCT CTG GGT ATG GAT CGG TAT CTT CTC ACC CTT CAC CCA GTG TGG TCC

Leu Leu Thr Leu His Pro Val Trp Ser

63 72 81 90 99 108

CAA AAG CAC CGA ACC TCA CAC TGG GCT TCC AGA GTC GTT CTG GGA GTC TGG CTC

Gln Lys His Arg Thr Ser His Trp Ala Ser Arg Val Val Leu Gly Val Trp Leu

117 126 135 144 153 162

TCT GCC ACT GCC TTC AGC GTG CCC TAT TTG GTT TTC AGG GAG ACA TAT GAT GAC

Ser Ala Thr Ala Phe Ser Val Pro Tyr Leu Val Phe Arg Glu Thr Tyr Asp Asp

171 180 189 198 207 216

CGT AAA GGA AGA GTG ACC TGC AGA AAT AAC TAC GCT GTG TCC ACT GAC TGG GAA

Arg Lys Gly Arg Val Thr Cys Arg Asn Asn Tyr Ala Val Ser Thr Asp Trp Glu

225 234 243 252 261 270

AGC AAA GAG ATG CAA ACA GTA AGA CAA TGG ATT CAT GCC ACC TGT TTC ATC AGC

Ser Lys Glu Met Gln Thr Val Arg Gln Trp Ile His Ala Thr Cys Phe Ile Ser

279 288 297 306 315 324

CGC TTC ATA CTG GGC TTC CTT CTG CCT TTC TTA GTC ATT GGC TTT TGT TAT GAA

Arg Phe Ile Leu Gly Phe Leu Leu Pro Phe Leu Val Ile Gly Phe Cys Tyr Glu

333 342 351 360 369 378

AGA GTA GCC CGC AAG ATG AAA GAG AGG GGC CTC TTT AAA TCC AGC AAA CCC TTC

Arg Val Ala Arg Lys Met Lys Glu Arg Gly Leu Phe Lys Ser Ser Lys Pro Phe

387 396 405 414 423 432

AAA GTC ACG ATG ACT GCT GTT ATC TCT TTT TTC TGT CCT GGC TTC CCT ACC ACA

Lys Val Thr Met Thr Ala Val Ile

TG 3'

5 0 / 7 9

FIGURE 50

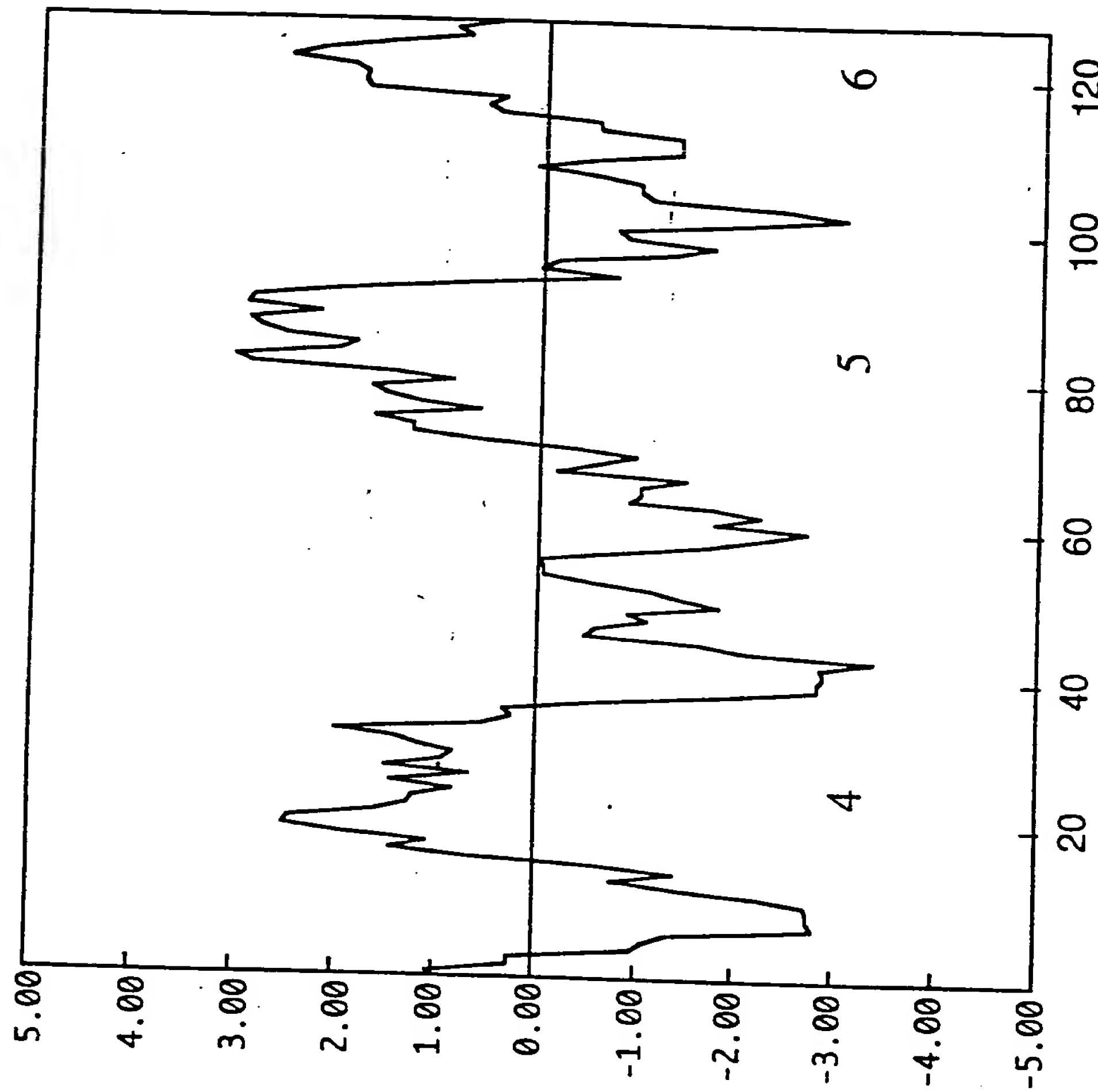


FIGURE 51

		5	1	7	9
1	LTLLHPVWESQ	KIERTSHWASR	VVLCMWSAT	AFSVPYLVFR	ETYDDR-K-G
1	ICVILHPVWAG	NERTVSIAMK	VTVQPMWAL	VITLPEVFL	TTVTTEP-N-G
1	VCVTHPVWEG	NERTVSIAMK	VTVQPMWAL	EQTRPVVIRV	TTVPGK-T-G
1	ICVILHPVWAG	NHRNVSIAKK	VTVGPWICAL	LLTLPVTVRV	TTLSHPRAPG
1	FLMKPIMCQ	KVRSIGIAMM	ACGVAWMLAL	LLTIPSFVYR	EAYKDFYS-E
1	LAVVHATNSQ	KPRKLLAEKV	VYVGWLPAV	LITPDLIYA	DI-KEV-D-E
10					
20					
30					
40					
50					
PMJ10					
B42009					
JC2014					
A46520					
A46525					
S28787					
51	RVTGRNNYAV	STDWESKEMQ	TYRQMIHATC	FISRFILGFL	LPFLVIGFCY
51	DTYQPFNEAS	WGG-TPEERL	KVATMLTAR	GIRFVIGFS	IPMSIVAVICY
51	TVACTENFSP	WTN-DPEKERI	KVAVAMLTVR	GIRFVIGFS	APMSIVAVSY
51	KMACTEDWSP	WTE-DPAEKI	KVAISMMFVR	GIRFVIGFS	TPMSIVAVCY
51	HIVCCGINYEG	GS--FPEKEA	VA-----	-ILRIMVGFV	TPLLTLNICY
51	RVTCDRFYIP-	SDLW-----L	VVFQFQE---	-----IVVGLL	LPGIVILSCY
60					
70					
80					
90					
100					
PMJ10					
B42009					
JC2014					
A46520					
A46525					
S28787					
110	ERVARKMKER	GLFKSSKPFK	VPMIAVI	...	150
101	GLTATKTHRK	GMFKSSRPLR	VLDAVVA	...	150
101	GLTATKTHKQ	GLIKSSRPLR	VLSFVAA	...	150
101	GLTATKTHRO	GLIKSSRPLR	VLSFVVA	...	150
101	TFLLRITWSR	KATRSIKTALK	VMMAVVI	...	150
101	CRISKLSHS	KGYQKRKALK	TTVILLI	...	150
120					
130					
140					
150					

FIGURE 52

5' CTG ACT GCT CTG GGG ACT GAC CGG TAT TTC AAG ATT GTG AAG CCC CTT TCC ACG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Phe Lys Ile Val Lys Pro Leu Ser Thr
 63 72 81 90 99 108
 TCC TTC ATC CAG TCT GTG AAC TAC AGC AAA CTC GTC TCG CTG GTG GTC TGG TTG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Ser Phe Ile Gln Ser Val Asn Tyr Ser Lys Leu Val Ser Leu Val Val Trp Leu
 117 126 135 144 153 162
 CTC ATG CTC CTC GCC GTC CCC AAC GTC ATT CTC ACC AAC CAG AGA GTT AAG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Leu Met Leu Leu Ala Val Pro Asn Val Ile Leu Thr Asn Gln Arg Val Lys
 171 180 189 198 207 216
 GAC GTG ACG CAG ATA AAA TGC ATG GAA CTT AAA AAC GAA CTG GGC CGC CAG TGG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Asp Val Thr Gln Ile Lys Cys Met Glu Leu Lys Asn Glu Leu Gly Arg Gln Trp
 225 234 243 252 261 270
 CAC AAG GCG TCA AAC TAC ATC TTT GTG GGC ATT TTC TGG CTT GTG TTC CTT TTG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 His Lys Ala Ser Asn Tyr Ile Phe Val Gly Ile Phe Trp Leu Val Phe Leu Leu
 279 288 297 306 315 324
 CTA ATC ATT TTC TAC ACT GCT ATC ACC AGG AAA ATC TTT AAG TCC CAC CTG AAA
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Leu Ile Ile Phe Tyr Thr Ala Ile Thr Arg Lys Ile Phe Lys Ser His Leu Lys
 333 342 351 360 369 378
 TCC AGA AAG AAT TCC ATC TCG GTC AAA AAG AAA TCT AGC CGC AAC ATC TTC AGC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Ser Arg Lys Asn Ser Ile Ser Val Lys Lys Lys Ser Ser Arg Asn Ile Phe Ser
 387 396 405 414
 ATC GTG TTT ATC CTC TGT TGG CCC CCC TAC CAC ATC 3'
 Ile Val

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FIGURE 53

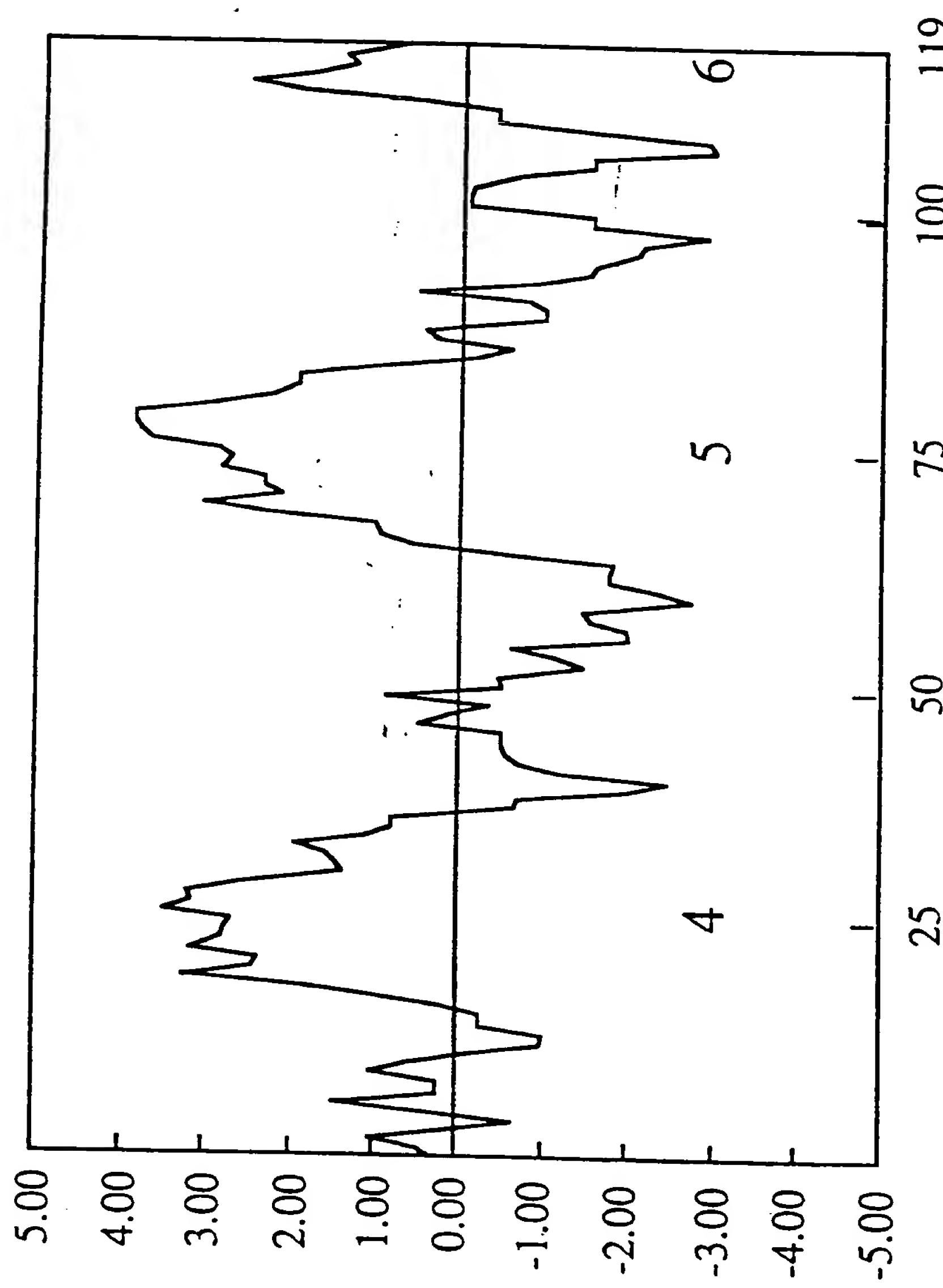


FIGURE 54

5	4	7	9
10	20	30	40
1 FKIVKPLSTS	FIQSVNYSKL	VSLVVNLML	ELAVPNVLT
1 LAIVVHATSP-	LIQKRHLVKF	YCIAMWLSV	ILALPILUR
1 YAVVHPLKAA	RYRRPFTVAKV	VNLGVWVESP	LVTLPVMFS
1 YAVVHPLRAA	TYRRPSVAKI	INLGVWLAISL	LVTLPVIAFA
50	50	50	50
50	50	50	50
50	50	50	50
50	50	50	50
60	70	80	90
51 KCME-LKONEL	GRQWHKASNY	IFVGIE-WLV	FLLILIFYTA
51 VCYEDVGNNT	SRL--RIVLRL	ILPQTEGFLV	FLLIMLFCYG
51 AGNM-LMPPEP	AQRWLVGFEV-	LYTFILMGEFL	PVGATCICV
51 AVAC-NLQWE	HPAWSAVFV-	VYTFILLGFLL	PVLATIGLCYL
100	100	100	100
100	100	100	100
100	100	100	100
100	100	100	100
110	120	130	140
101 LKSRKNSI-S	VKKKSRSRNIF	S--IV	150
101 MG---QKHR	AMR---VIE	AVVLV	150
101 EKAGWQQRR	SERKTTLMVM	MVVVV	150
101 ERAGWQQRR	SERKTTRLVL	MVVVV	150

5 5 / 7 9

FIGURE 55

5' 9 18 27 36 45 54
GCC ACC AAC GTG TTC ATC CTG TGT CTG GTG GAC CTG CTG GCT GCC CTG ACC CTC

Val Asp Leu Leu Ala Ala Leu Thr Leu

63 72 81 90 99 108
ATG CCT CTG GCC ATG CTC TCC AGC TCC GCC CTC TTT GAC CAC GCC CTC TTT GGG

Met Pro Leu Ala Met Leu Ser Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly

117 126 135 144 153 162
GAG GTG GCC TGC CGC CTC TAC TTG TTC CTG AGC GTC TGC TTT GTC AGC CTG GCC

Glu Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu Ala

171 180 189 198 207 216
ATC CTC TCG GTG TCC GCC ATC AAT GTG GAG CGC TAC TAT TAT GTG GTC CAC CCC

Ile Leu Ser Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val Val His Pro

225 234 243 252 261 270
ATG CGC TAT GAG GTG CGC ATG AAA CTG GGG CTG GTG GCC TCT GTG CTG GTG GGC

Met Arg Tyr Glu Val Arg Met Lys Leu Gly Leu Val Ala Ser Val Leu Val Gly

279 288 297 306 315 324
GTG TGG GTG AAG GCC CTG GCC ATG GCT TCT GTG CCA GTG TTG GGA AGG GTG TCC

Val Trp Val Lys Ala Leu Ala Met Ala Ser Val Pro Val Leu Gly Arg Val Ser

333 342 351 360 369 378
TGG GAG GAA GGC CCT CCC AGT GTC CCC CCA GGC TGT TCA CTC CAA TGG AGC CAC

Trp Glu Glu Gly Pro Pro Ser Val Pro Pro Gly Cys Ser Leu Gln Trp Ser His

387 396 405 414 423 432
AGT GCC TAC TGC CAG CTT TTC GTG GTG GTC TTC GCC GTC CTC TAC TTC CTG CTG

Ser Ala Tyr Cys Gln Leu Phe Val Val Phe Ala Val Leu Tyr Phe Leu Leu

441 450 459 468 477 486
CCC CTG CTC CTC ATC CTT GTG GTC TAC TGC AGC ATG TTC CGG GTG GCT CGT GTG

Pro Leu Leu Leu Ile Leu Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val

495 504 513 522 531 540
GCT GCC ATG CAG CAC GGG CCG CTG CCC ACG TGG ATG GAG ACG CCC CGG CAA CGC

Ala Ala Met Gln His Gly Pro Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg

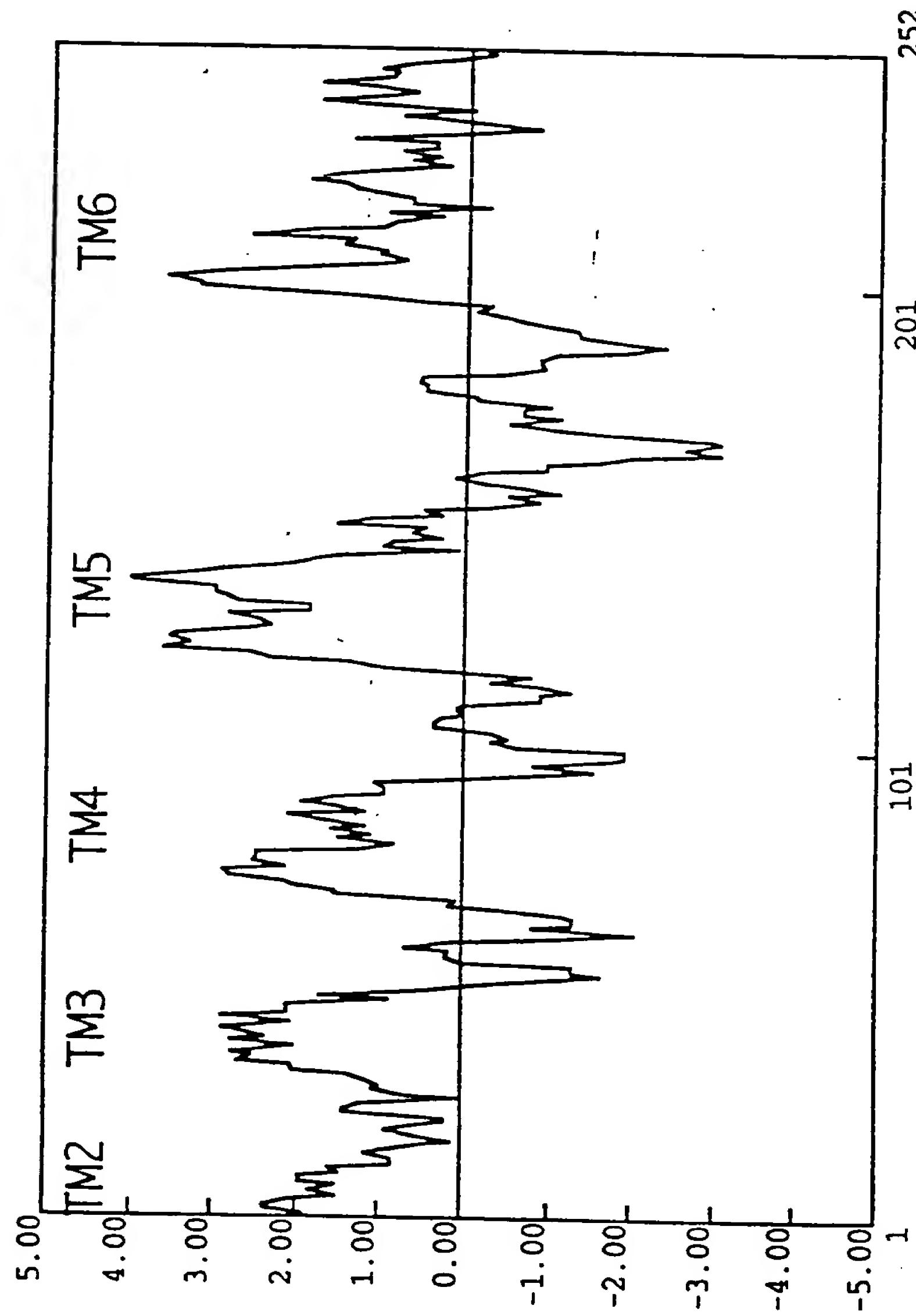
FIGURE 56

549	558	567	576	585	594
TCC	GAG	TCT	CTC	AGC	CGC
-----	-----	-----	-----	-----	-----
Ser	Glu	Ser	Leu	Ser	Ser
503	612	621	630	639	648
ACC	ACC	CCT	CAC	CGG	ACG
-----	-----	-----	-----	-----	-----
Thr	Thr	Pro	His	Arg	Thr
657	666	675	684	693	702
GTG	GGA	GGA	CAG	TTC	CTG
-----	-----	-----	-----	-----	-----
Val	Gly	Gly	Gln	Phe	Leu
711	720	729	738	747	756
GTG	GCC	CTG	AGC	GCT	CAC
-----	-----	-----	-----	-----	-----
Val	Ala	Leu	Ser	Ala	Gln
765	774	783	792	801	810
TGG	ATT	GGC	TAC	TTC	TTC
-----	-----	-----	-----	-----	-----
Trp	Ile	Gly	Tyr	Phe	Cys

TCC GAG TCT CTC AGC AGC CGC TCC ACT ATG GTC ACC ACC AGC TCG GGG GCC CCG CAG
 Ser Glu Ser Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro Gln
 ACC ACC CCT CAC CGG ACG TTT GGC GGA GGG AAG GCA GCA GTG GTC CTC CTG GCT
 Thr Thr Pro His Arg Thr Phe Gly Gly Lys Ala Ala Val Val Leu Leu Ala
 GTG GGA GGA CAG TTC CTG CTC TGT TGG TTG CCC TAC TTC TCC TTC CAC CTC TAT
 Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe Ser Phe His Leu Tyr
 GTG GCC CTG AGC GCT CAG CCC ATT GCA GCG GGG CAG GTG GAG AAC GTG GTG ACC
 Val Ala Leu Ser Ala Gln Pro Ile Ala Ala Gly Gln Val Glu Asn Val Val Thr
 TGG ATT GGC TAC TTC TGC TTC ACC TCC AAC CCT CTC CTC TAT TCC TTC CTC CCT 3'
 Trp Ile Gly Tyr Phe Cys Phe Thr Ser

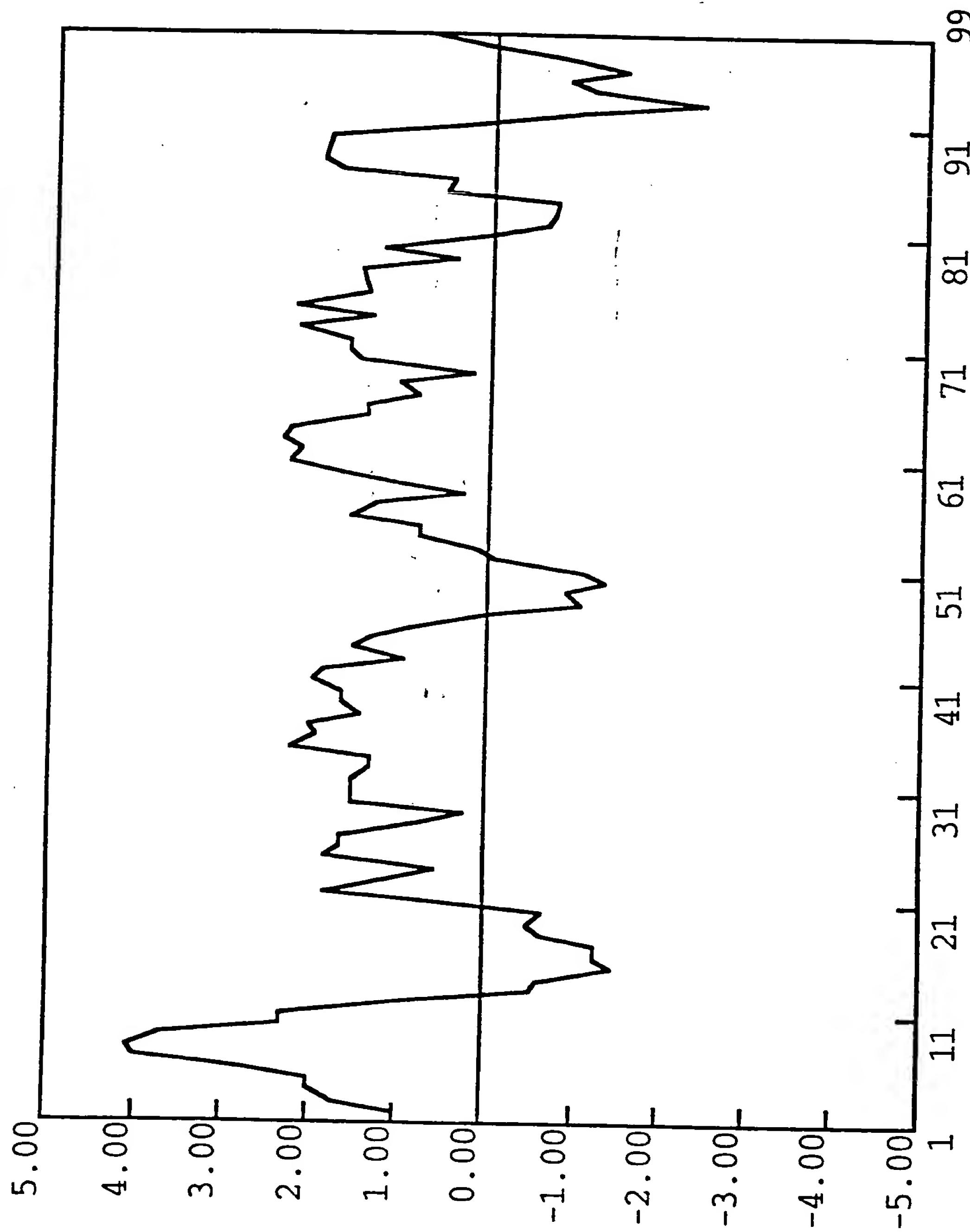
5 7 / 7 9

FIGURE 57



5 8 / 7 9

FIGURE 58



5 9 / 7 9

FIGURE 59

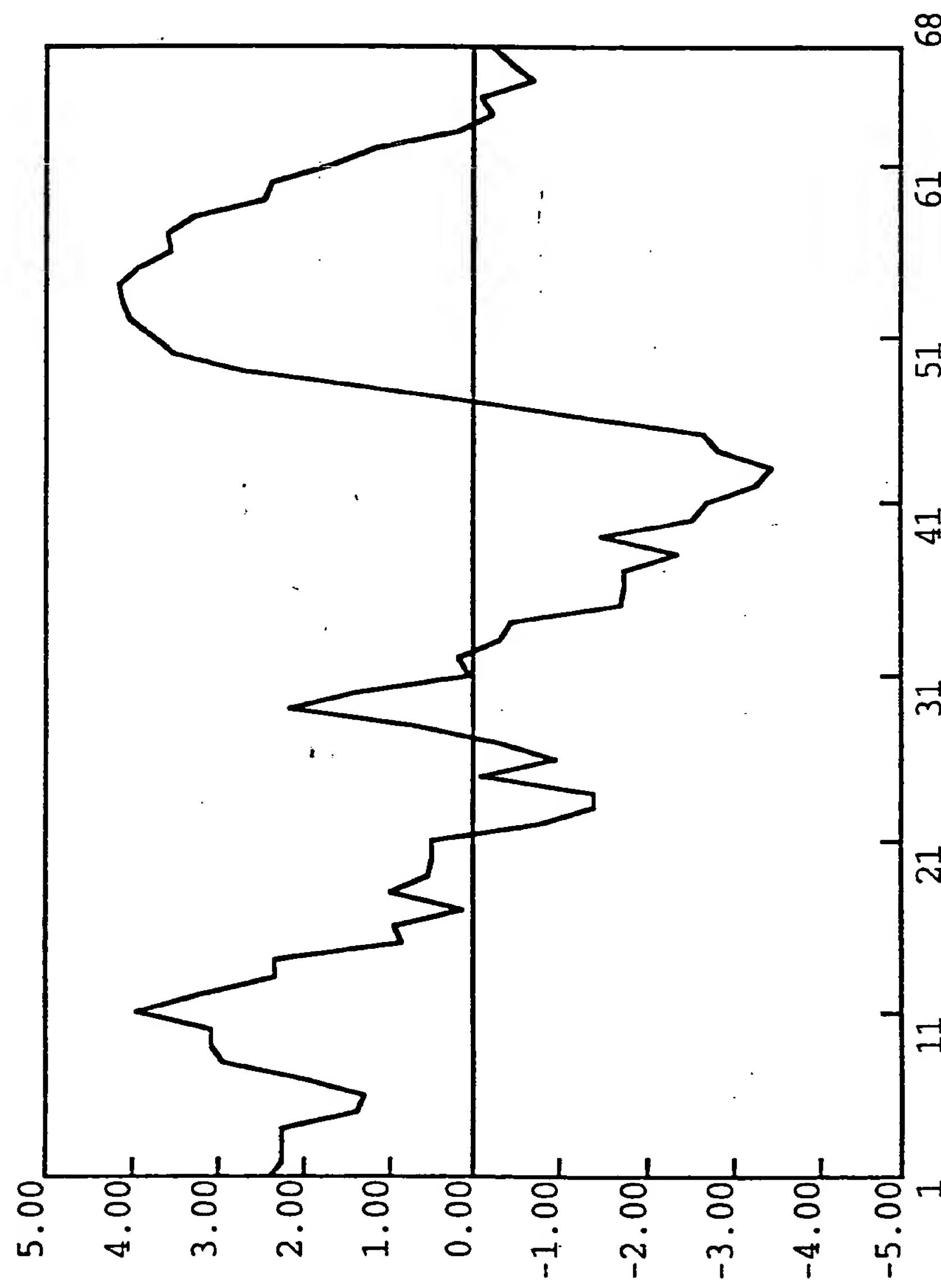


FIGURE 60

FIGURE 62

5. 9 18 27 36 45 54
 CTG TGT GTC ATC GCG GTG GAT AGG TAC GTG GTT CTG GTG CAC CCG CTA CGT CGG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu Cys Val Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg Arg
 63 72 81 90 99 108
 CGC ATT TCA CTG AGG CTC AGC GCG TAC GCG GTG CTG GGC ATC TGG GCT CTA TCT
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser
 117 126 135 144 153 162
 GCA GTG CTG GCG CTG CCG GCC GCG GTG CAC ACC TAC CAT GTG GAG CTC AAG CCC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro
 171 180 189 198 207 216
 CAC GAC GTG AGC CTC TGC GAG GAG TTC TGG GGC TCG CAG GAG CGC CAA CGC CAG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
His Asp Val Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln
 225 234 243 252 261 270
 ATC TAC GCC TGG GGG CTG CTT CTG GGC ACC TAT TTG CTC CCC CTG CTG GCC ATC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ile Tyr Ala Trp Gly Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala Ile
 279 288 297 306 315 324
 CTC CTG TCT TAC GTA CGG GTG TCA GTG AAG CTG AGG AAC CGC GTG GTG CCT GGC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly
 333 342 351 360 369 378
 AGC GTG ACC CAG AGT CAA GCT GAC TGG GAC CGA GCG CGT CGC CGC ACT TTC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe
 387 396 405 414 423 432
 TGT CTG CTG GTG GTG GTG GTA GTG TTC ACG CTC TGC TGG CTG CCC TTC TAC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Cys Leu Leu Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Tyr

CT 3'

--

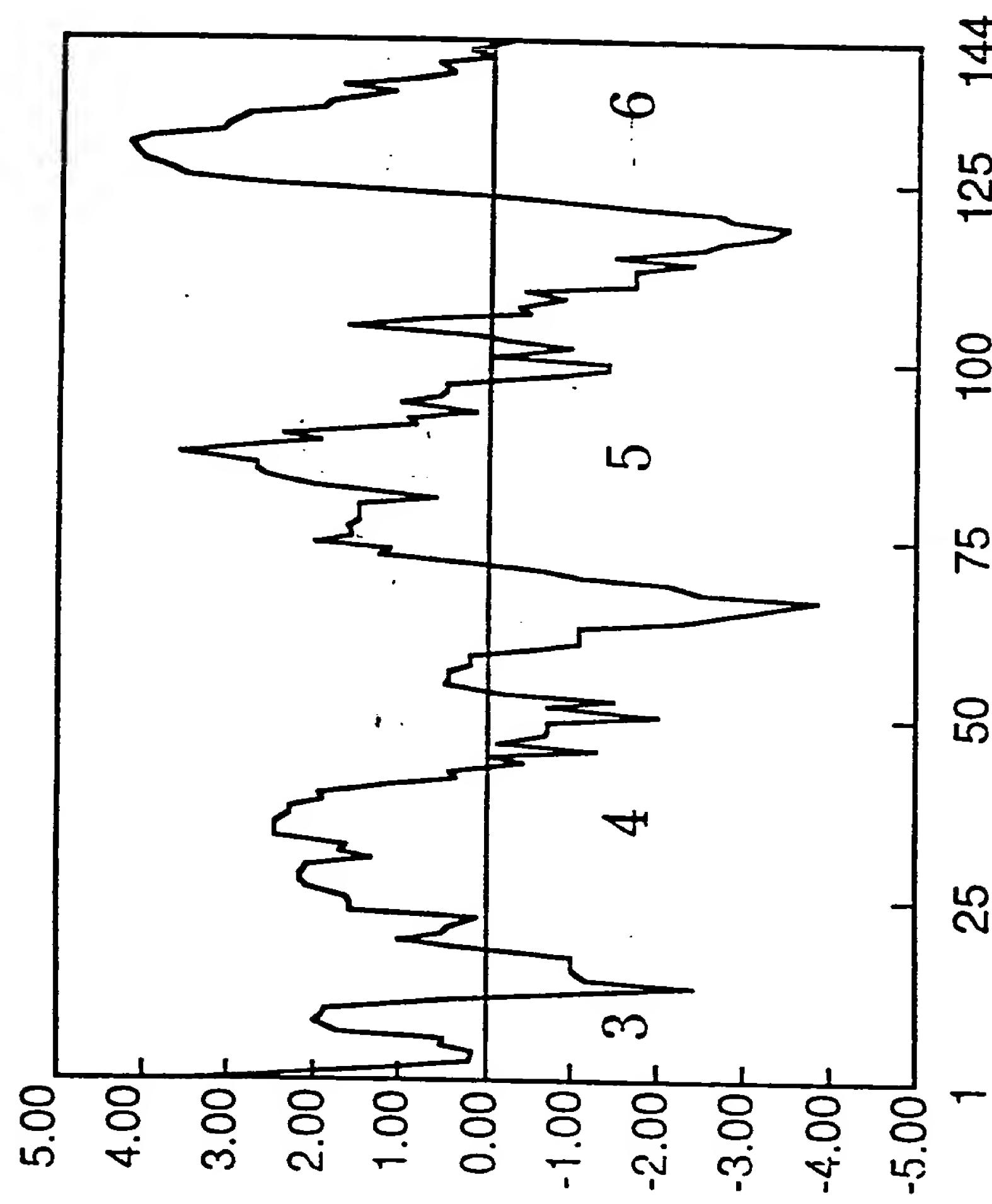
—

FIGURE 63

p19P2 PG3-2 / PG1-10 p5S38	1	VGMVGNVILLV VGMVGNVILLV	10	LVIAARVRRHH EVIAARVRRHH	20	NVTNEELIIGNL NVTNEELIIGNL	30	ALSDVILMCTA AISDVILMCTA	40	CVPILTLAYAF CVPILTLAYAF	50
	1 -79	51	EPRCGWVFEGGG EPRGWVFEGGG	60	ECHLVEFLOP ECHEVFELQ	70	VTIVYVSVETIL VTIVYVSVETIL	80	TTIAVIDRYAVV TTIAVIDRYAVV	90
	51	51 -29	51 -29	101 -101	110 101 22	120 IWWLSAVIAL IWWLSAVIAL	130
p19P2 PG3-2 / PG1-10 p5S38	101 -29	101 -101	110 IWWLSAVIAL IWWLSAVIAL	120 IWWLSAVIAL IWWLSAVIAL	130 IWWLSAVIAL IWWLSAVIAL	140
	110 -29	110 -101	120 IWWLSAVIAL IWWLSAVIAL	130 IWWLSAVIAL IWWLSAVIAL	140 IWWLSAVIAL IWWLSAVIAL	150
	120 -29	120 -101	130 IWWLSAVIAL IWWLSAVIAL	140 IWWLSAVIAL IWWLSAVIAL	150 IWWLSAVIAL IWWLSAVIAL	160
p19P2 PG3-2 / PG1-10 p5S38	130 -29	130 -101	140 IWWLSAVIAL IWWLSAVIAL	150 IWWLSAVIAL IWWLSAVIAL	160 IWWLSAVIAL IWWLSAVIAL	170
	140 -29	140 -101	150 IWWLSAVIAL IWWLSAVIAL	160 IWWLSAVIAL IWWLSAVIAL	170 IWWLSAVIAL IWWLSAVIAL	180
	150 -29	150 -101	160 IWWLSAVIAL IWWLSAVIAL	170 IWWLSAVIAL IWWLSAVIAL	180 IWWLSAVIAL IWWLSAVIAL	190
p19P2 PG3-2 / PG1-10 p5S38	160 -29	160 -101	170 IWWLSAVIAL IWWLSAVIAL	180 IWWLSAVIAL IWWLSAVIAL	190 IWWLSAVIAL IWWLSAVIAL	200
	170 -29	170 -101	180 IWWLSAVIAL IWWLSAVIAL	190 IWWLSAVIAL IWWLSAVIAL	200 IWWLSAVIAL IWWLSAVIAL	210
	180 -29	180 -101	190 IWWLSAVIAL IWWLSAVIAL	200 IWWLSAVIAL IWWLSAVIAL	210 IWWLSAVIAL IWWLSAVIAL	220
p19P2 PG3-2 / PG1-10 p5S38	190 -29	190 -101	200 IWWLSAVIAL IWWLSAVIAL	210 IWWLSAVIAL IWWLSAVIAL	220 IWWLSAVIAL IWWLSAVIAL	230
	200 -29	200 -101	210 IWWLSAVIAL IWWLSAVIAL	220 IWWLSAVIAL IWWLSAVIAL	230 IWWLSAVIAL IWWLSAVIAL	240
	210 -29	210 -101	220 IWWLSAVIAL IWWLSAVIAL	230 IWWLSAVIAL IWWLSAVIAL	240 IWWLSAVIAL IWWLSAVIAL	250
p19P2 PG3-2 / PG1-10 p5S38	220 -29	220 -101	230 IWWLSAVIAL IWWLSAVIAL	240 IWWLSAVIAL IWWLSAVIAL	250 IWWLSAVIAL IWWLSAVIAL	260
	230 -29	230 -101	240 IWWLSAVIAL IWWLSAVIAL	250 IWWLSAVIAL IWWLSAVIAL	260 IWWLSAVIAL IWWLSAVIAL	270
	240 -29	240 -101	250 IWWLSAVIAL IWWLSAVIAL	260 IWWLSAVIAL IWWLSAVIAL	270 IWWLSAVIAL IWWLSAVIAL	280

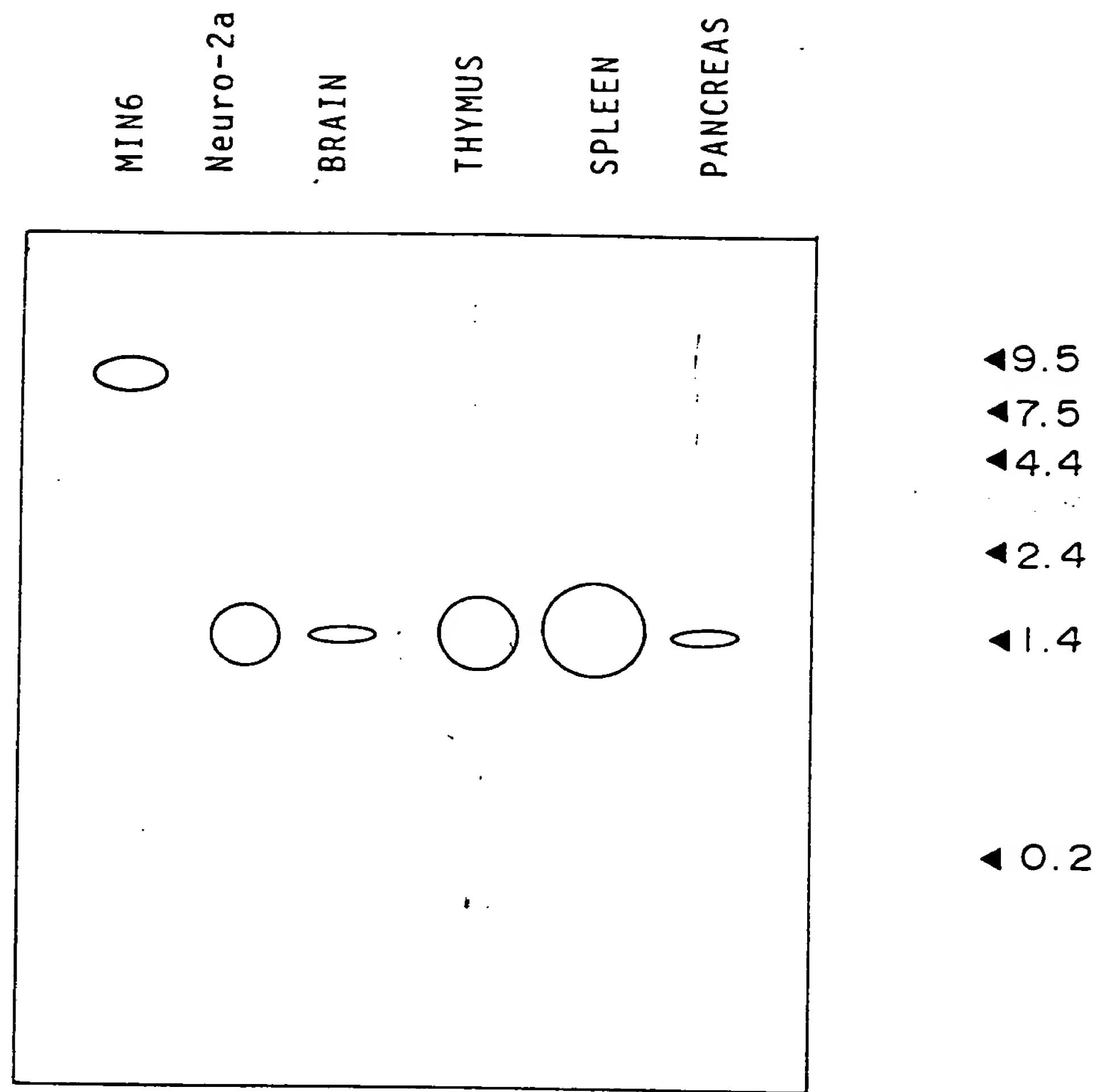
6 4 / 7 9

FIGURE 64



6 5 / 7 9

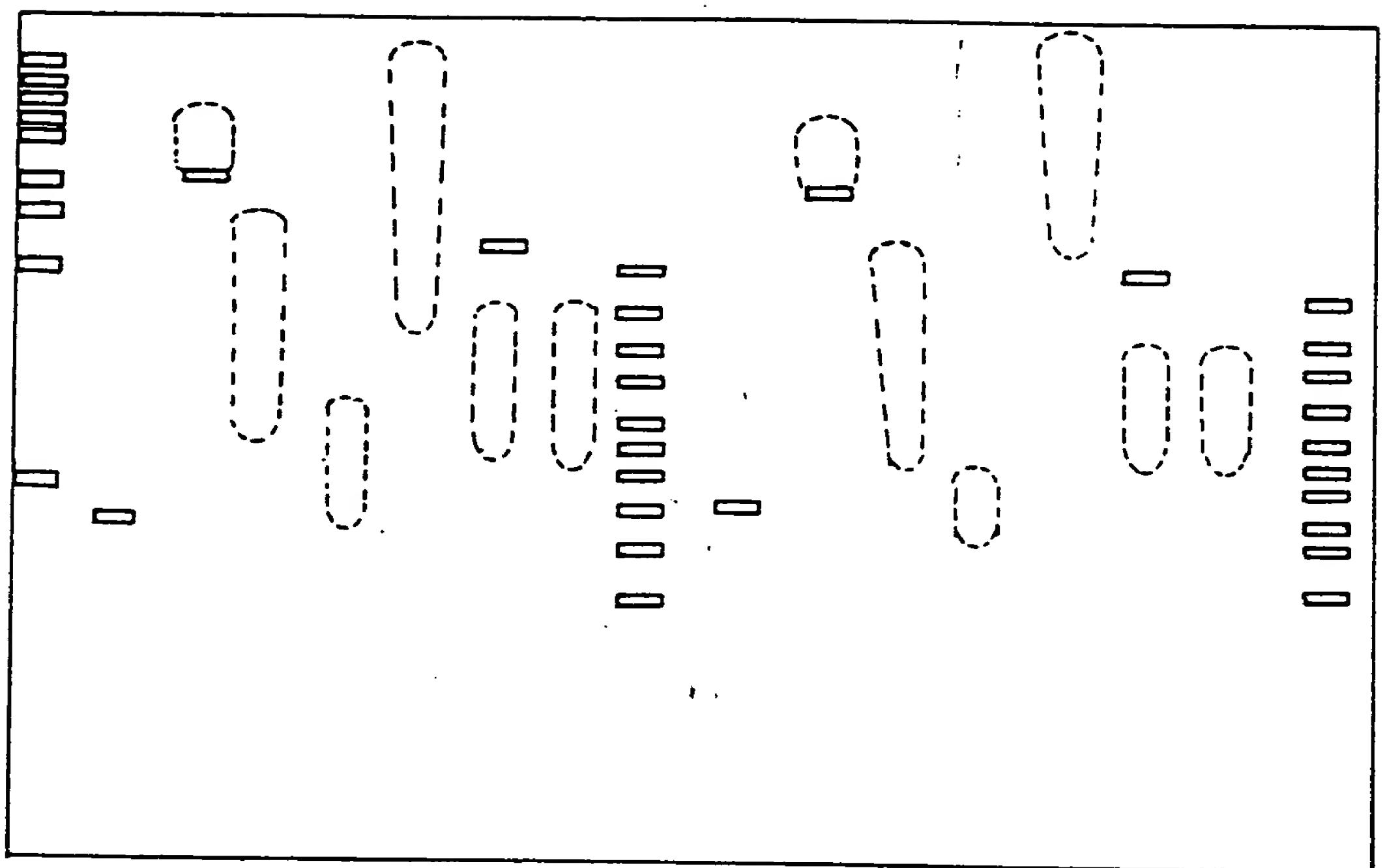
FIGURE 65



6 6 / 7 9

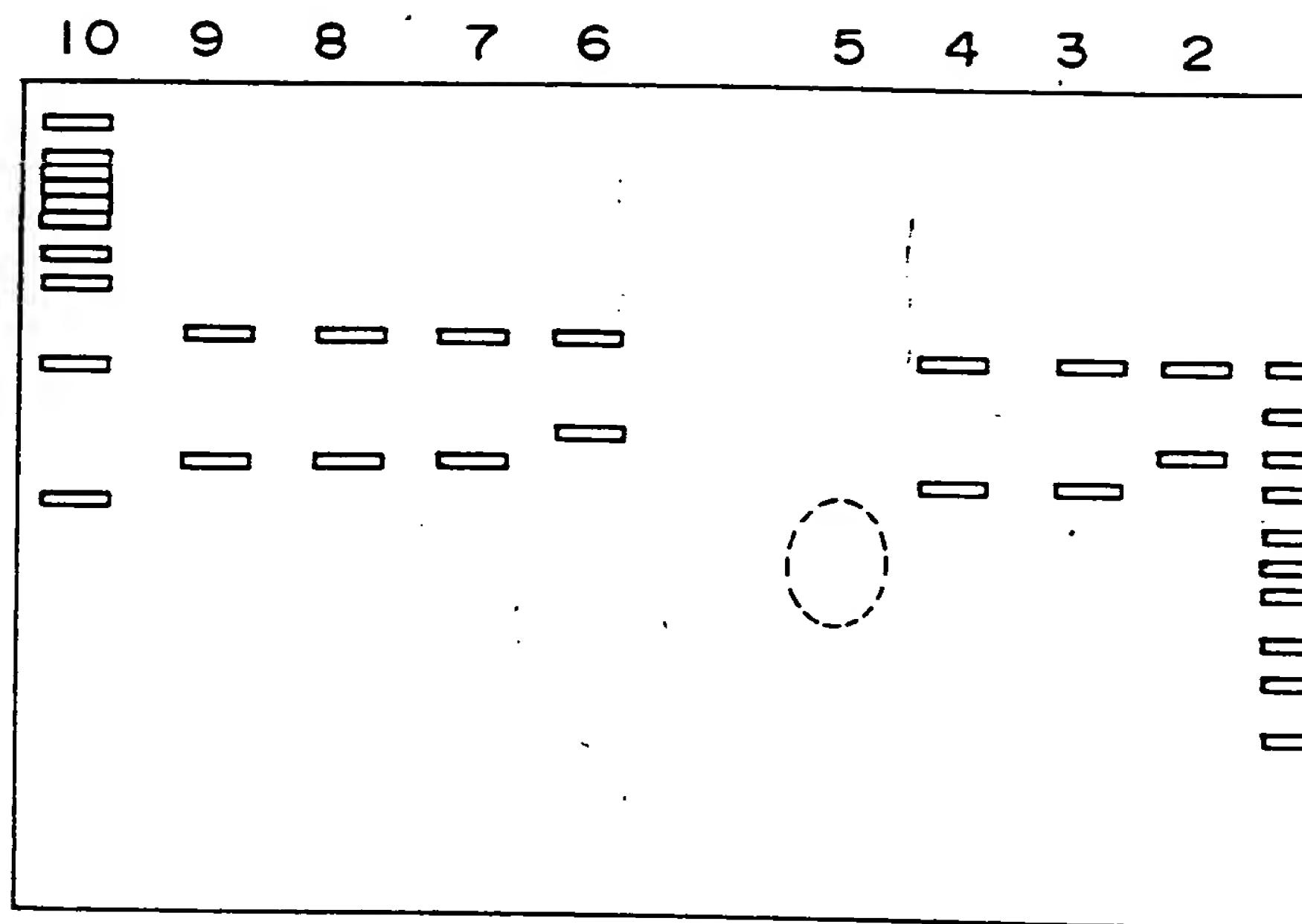
FIGURE 66

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17



6 7 / 7 9

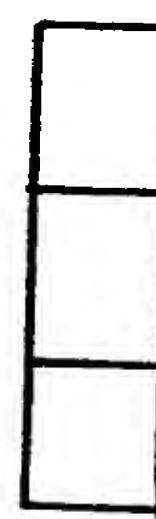
FIGURE 67



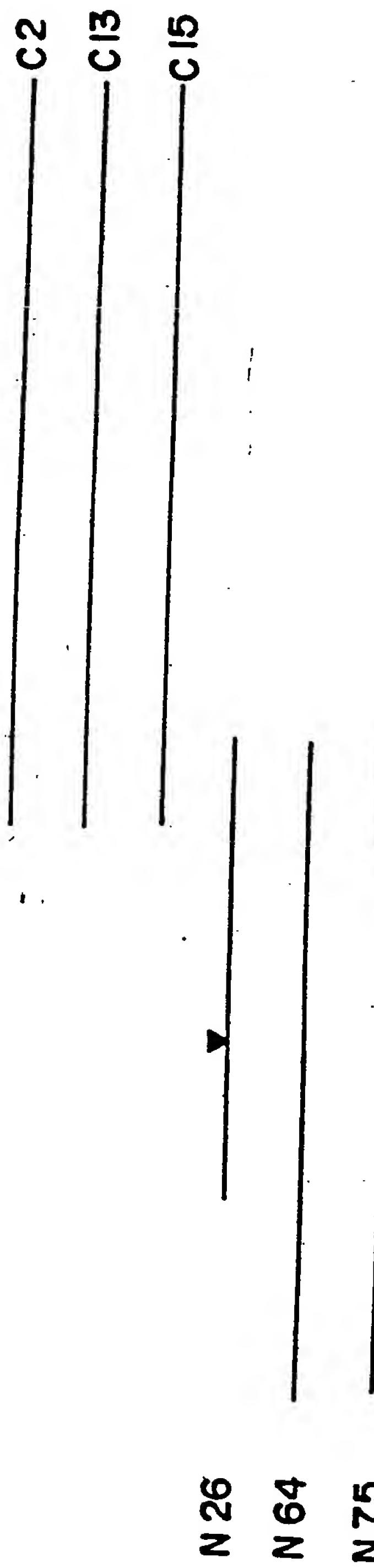
6 8 / 7 9

FIGURE 68

3H2-17 FRAGMENT



①② ③④



C2 SPLEEN DERIVED C13 SPLEEN DERIVED C15 THYMUS DERIVED
N75 SPLEEN DERIVED N26 THYMUS DERIVED N64 THYMUS DERIVED

▼ PCR ERROR SITE

FIGURE 69

1	GAGCCTAGGAAAGGCTGACAGGCAGTATGGAGCAGGACAATGCCACCATCCAGGCTCCA	60
1	MetGluGlnAspAspGlyThrIleGlnAlaPro	11
61	GGCTTGCCGCCACCACCTGGCTACCGTGAGGATTCAAGCGACTGCTGCTAACCCCG	120
11	GlyLeuProProThrThrCysValTyrArgGluAspPheLysArgLeuLeuThrPro	31
121	GTATACTCGGTGGTGGCTGGCTGGCTGCCACTGACATCTGGCTATTGCCAGATC	180
31	ValTyrSerValValLeuValValGlyLeuProLeuAsnIleCysValIleAlaGlnIle	51
181	TGGCGATCCCGCCGGACCCTGACCCGTTCCGCTGTGTACACCCCTGAACCTGGCACTGGCG	240
51	CysAlaSerArgArgThrLeuThrArgSerAlaValTyrThrLeuAsnLeuAlaLeuAla	71
241	GACCTGATGTATGCCTGTTCACTACCCCTACTTATCTATAACTACGCCAGAGGGGACCAC	300
71	AspLeuMetTyrAlaCysSerLeuProLeuLeuIleTyrAsnTyrAlaArgGlyAspHis	91
301	TGGCCCTTCGGAGACCTGGCTGCCGCTTGTACGCTTCCTCTCTATGCCAATCTACAT	360
91	TrpProPheGlyAspLeuAlaCysArgPheValArgPheLeuPheTyrAlaAsnLeuHis	111
361	GGCAGCATCTGTTCTCACCTGCATTAGCTTCCAGCGCTACCTGGCATCTGCCACCC	420
111	GlySerIleLeuPheLeuThrCysIleSerPheGlnArgTyrLeuGlyIleCysHisPro	131
421	CTGGCTTCCCTGGCACAAAGCTGGAGGTGGCCGTGCTGGTAGTGTGTGGAGTCGTG	480
131	LeuAlaSerTyrHisLysArgGlyGlyArgArgAlaAlaTrpValValCysGlyValVal	151
481	TGGCTGGCTGTGACAGCCCAGTGCCTGCCACGGCAGTCTTGCTGCCACAGGCATCCAG	540
151	TrpLeuAlaValThrAlaGlnCysLeuProThrAlaValPheAlaAlaThrGlyIleGln	171
541	CGCAACCGCACTGTGTGCTACGACCTGAGCCCACCCATCTGTCTACTCGCTACCTGCC	600
171	ArgAsnArgThrValCysTyrAspLeuSerProProIleLeuSerThrArgTyrLeuPro	191
601	TATGGTATGGCCCTCACGGTCATGGCTTCTGCTGCCCTCATAGCCTTACTGGCTTGT	660
191	TyrGlyMetAlaLeuThrValIleGlyPheLeuLeuProPheIleAlaLeuAlaCys	211
661	TATTGTGGCAAGGCCCGCCGCTGTGTGGCCAGGATGGCCCAGCAGGTCTGTGGCCCAA	720
211	TyrCysArgMetAlaArgArgLeuCysArgGlnAspGlyProAlaGlyProValAlaGln	231
721	GAGCGGGCGAGCAAGGCGGCTCGTATGGCTGTGGTGGCAGCTGTCTTGCCATCAGC	780
231	GluArgArgSerLysAlaAlaArgMetAlaValValAlaAlaValPheAlaIleSer	251
781	TTCCTGCCCTTCCACATACCAAGACAGCCTACTTGGCTGTGCGCTCCAGGCCGGTGT	840
251	PheLeuProPheHisIleThrLysThrAlaTyrLeuAlaValArgSerThrProGlyVal	271
841	TCTTGCCCTGTGCTGGAGACCTTCGCTGCTGCCACAAAGGCAGTCGGCCCTTCGCCAGT	900
271	SerCysProValLeuGluThrPheAlaAlaAlaTyrLysGlyThrArgProPheAlaSer	291
901	GTCAACAGTGTCTGGACCCCATTCTCTTCTACTTCACACAAACAGAAGTTCGGCGGCAA	960
291	ValAsnSerValLeuAspProIleLeuPheTyrPheThrGlnGlnLysPheArgArgGln	311
961	CCCCACGATCTCTACAGAGGCTCACAGCCAAGTGGCAGAGGCAGAGAGTCTGAGGCC	1020
311	ProHisAspLeuLeuGlnArgLeuThrAlaLysTrpGlnArgGlnArgVal***	329

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FIGURE 70

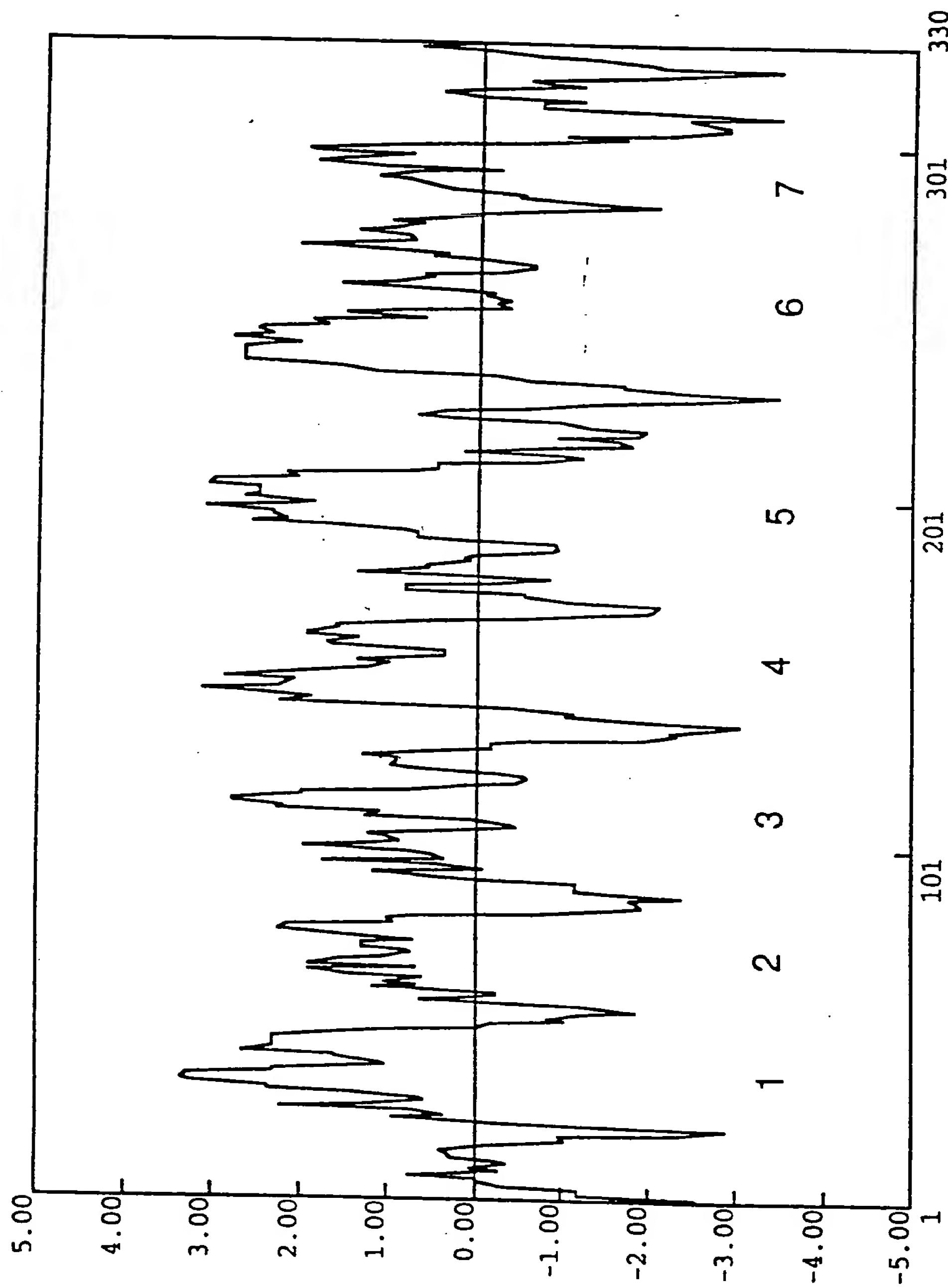


FIGURE 71

	10	20	30	40	50	
75+13, CODING						
P2UR_MOUSE	1 SEQD-----	--NGTIIQAGG	PP-----	-TT-SVYR-B	DEKRLLELTP-	50
P2YR_CHICK	1 MAAADLEPANS	TINGWEGDE	EGY-----	--KCRFN-B	DEKVVEL-B-	50
	1 VTEALISAAAL	--NGT-B-EE	ELAGGWAAGN	ATTKCSLTKT	GEQFYYL-BT	50
75+13, CODING						
P2UR_MOUSE	51 V-YSWVLWG	-E-ENICVIA	QI--CASRRT	LTR-SAVVIL	MLALADLYA	100
P2YR_CHICK	51 VSYGVVCVL-C	-E-CMVVALY	-ISLG-RLKU	WAA-SITTYIE	HEAVSESEVA	100
	51 V-YILVFTTS	PLG-NSVIAW	M-E-VFHMEP	MSGIS-VYME	MLALADFLYV	100
75+13, CODING						
P2UR_MOUSE	101 CSLPLLIYNY	ARG-DHWPFG	ELACRFVRFL	SYANL-GSIL	FLTCISFORY	150
P2YR_CHICK	101 ASLPLLYYYY	ARG-DHWPFS	TWLCKLVRFL	SYTNLYCSIL	FLTCISVHRC	150
	101 LTLPALIFYY	FNKTE-KIEG	DVMCKLQRFI	SHVANLYGSIL	FLTCISVHRY	150
75+13, CODING						
P2UR_MOUSE	151 EGICHEPLASH	HKRCGP-SAA	WVVCGVVWLA	VTAQCL-EPA	VPAAA-IGIQR	200
P2YR_CHICK	151 EGVLRPLHSL	--EWRARM	RRVAAVWWVI	VLA-COA PVL	YFTT-IVSVER	200
	151 TGWHPLKSL	G-SLAKCN-A	VYVSSLWVAL	WAVIA-PIL	-EYSGIGVRR	200
75+13, CODING						
P2UR_MOUSE	201 NRT-VCVLS	PPT-E-SRY	LPVGVVALIV	GRLLPEALL	ACVCRMARRL	250
P2YR_CHICK	201 TS-ITC-EDTS	ARE-IFSHFV	A-YSSVMLGL	LFAVPFSTVII	VCVVLMARRL	250
	201 NKTTTCYDIT	ACSYTFSYEV	--YSHCTIVF	MFCIPFTVII	CCYGLIVVKAL	250
75+13, CODING						
P2UR_MOUSE	251 CROGGPA-CP	VAQERRSAAA	--RMAVVA	VFAI SELPFH	ITKTAVALVR	300
P2YR_CHICK	251 -LR--PAYCF	TGGIPRAKRK	SVITIALVIA	VFALELPPFH	VTIRILVYSFH	300
	251 IYKD-LDNSP	---L-PRK--	STYLVIIIVL	VFAVSMPPFH	VMKILNLRAR	300
75+13, CODING						
P2UR_MOUSE	301 STP---GVSC	PVLETFAAY	RGTERPFASVN	SVLDPICFYF	TQOKERROPH	350
P2YR_CHICK	301 SLD---LSC	HTLNAINMAY	KIIPPEASAN	SCDPPVNL	AGORLVRFAR	350
	301 -LDFQTPQMC	AFNDKVVAY	QVIRGLASLN	SCVDPLVYEL	AGDTERRLS	350
75+13, CODING						
P2UR_MOUSE	351 ELLQRLTAKW	QR,PRV*	400
P2YR_CHICK	351 DAKPPTEPTP	SICARRKLGL	HRPNRTVRKD	LSVSSDDSR	TESTPAGSET	400
	351 RAIRKSSRRS	EIPNVQSKSEE	MTLNLTEYK	QNGDTSL	400
75+13, CODING						
P2UR_MOUSE	401	450
P2YR_CHICK	401 KDIRL.....	450
	401	450

FIGURE 72

9 18 27 36 45 54
 5' GCC ACC AAC GTG TTC ATC CTG TCA CTG GCC GAT GTG CTG GTG ACA GCC ATC TGC
 --- --- --- --- --- ---
 Ala Asp Val Leu Val Thr Ala Ile Cys

63 72 81 90 99 108
 CTG CCG GCC AGT CTG CTG GTA GAC ATC ACG GAA TCC TGG CTC TTT GGC CAT GCC
 --- --- --- --- --- ---
 Leu Pro Ala Ser Leu Leu Val Asp Ile Thr Glu Ser Trp Leu Phe Gly His Ala

117 126 135 144 153 162
 CTC TGC AAG GTC ATC CCC TAT CTA CAG GCC GTG TCC GTG TCA GTG GTC GTG CTG
 --- --- --- --- --- ---
 Leu Cys Lys Val Ile Pro Tyr Leu Gln Ala Val Ser Val Ser Val Val Leu

171 180 189 198 207 216
 ACT CTC AGC TCC ATC GCC CTG GAC CGC TGG TAC GCC ATC TGC CAC CCG CTG TTG
 --- --- --- --- --- ---
 Thr Leu Ser Ser Ile Ala Leu Asp Arg Trp Tyr Ala Ile Cys His Pro Leu Leu

225 234 243 252 261 270
 TTC AAG AGC ACT GCC CGG CGC GCC CGC GGC TCC ATC CTC GGC ATC TGG GCG GTG
 --- --- --- --- --- ---
 Phe Lys Ser Thr Ala Arg Arg Ala Arg Gly Ser Ile Leu Gly Ile Trp Ala Val

279 288 297 306 315 324
 TCG CTG GCT GTC ATG GTG CCT CAG GCT GCT GTC ATG GAG TGT AGC AGC GTG CTG
 --- --- --- --- --- ---
 Ser Leu Ala Val Met Val Pro Gln Ala Ala Val Met Glu Cys Ser Ser Val Leu

333 342 351 360 369 378
 CCC GAG CTG GCC AAC CGC ACC CGC CTC CTG TCT GTC TGT GAT GAG CGC TGG GCA
 --- --- --- --- --- ---
 Pro Glu Leu Ala Asn Arg Thr Arg Leu Leu Ser Val Cys Asp Glu Arg Trp Ala

387 396 405 414 423 432
 GAC GAC CTG TAC CCC AAG ATC TAC CAC AGC TGC TTC ATT GTC ACC TAC CTG
 --- --- --- --- --- ---
 Asp Asp Leu Tyr Pro Lys Ile Tyr His Ser Cys Phe Phe Ile Val Thr Tyr Leu

441 450 459 468 477 486
 GCC CCA CTG GGC CTC ATG GCC ATG GGC TAT TTC CAG ATC TTC CGC AAG CTC TGG
 --- --- --- --- --- ---
 Ala Pro Leu Gly Leu Met Ala Met Ala Tyr Phe Gln Ile Phe Arg Lys Leu Trp

495 504 513 522 531 540
 GGC CGC CAG ATC CCC GGC ACC ACC TCG GCC CTG GTG CGC AAC TGG AAG CGG CCC

FIGURE 73

Gly Arg Gln Ile Pro Gly Thr Thr Ser Ala Leu Val Arg Asn Trp Lys Arg Pro
 549 558 567 576 585 594
 TCA GAC CAG CTG GAC GAC CAG GGC CAG GGC CTG AGC TCA GAG CCC CAG CCC CGG

 Ser Asp Gln Leu Asp Asp Gln Gly Gln Gly Leu Ser Ser Glu Pro Gln Pro Arg
 603 612 621 630 639 648
 GCC CGC GCC TTC CTG GCC GAG GTG AAA CAG ATG CGA GCC CGG AGG AAG ACG GCC

 Ala Arg Ala Phe Leu Ala Glu Val Lys Gln Met Arg Ala Arg Arg Lys Thr Ala
 657 666 675 684 693 702
 AAG ATG CTG ATG GTG GTG CTG CTG GTC TTC GCC CTC TGC TAC CTG CCC ATC AGT

 Lys Met Leu Met Val Val Leu Val Phe Ala Leu Cys Tyr Leu Pro Ile Ser
 711 720 729 738 747 756
 GTC CTC AAC GTC CTC AAG AGG GTC TTC GGG ATG TTC CGC CAA GCC AGC GAC CGA

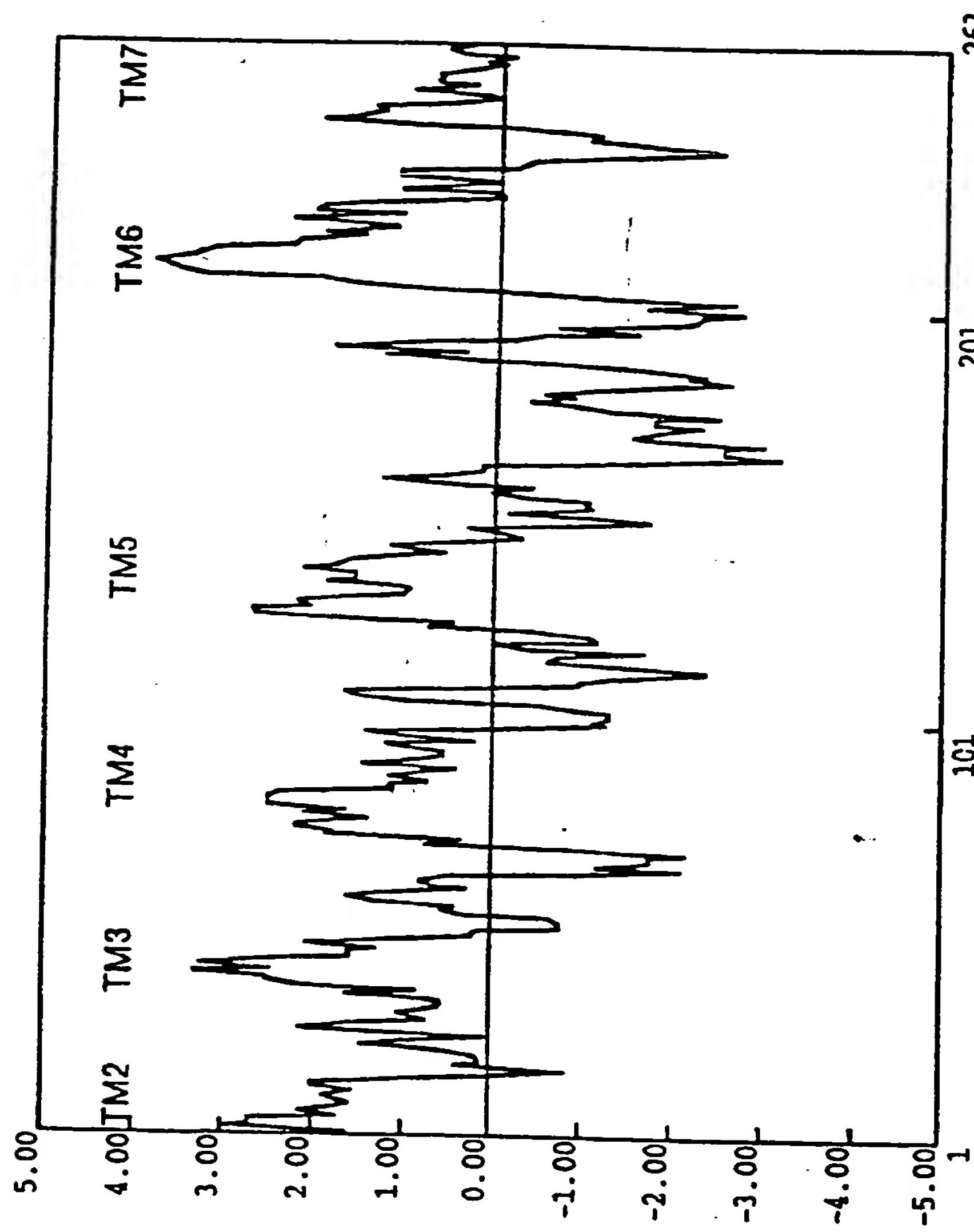
 Val Leu Asn Val Leu Lys Arg Val Phe Gly Met Phe Arg Gln Ala Ser Asp Arg
 765 774 783 792 801 810
 GAG GCC ATC TAC GCC TGC TTC ACC TTC TCC CAC TGG CTG GTG TAC GCC AAC AGC

 Glu Ala Ile Tyr Ala Cys Phe Thr Phe Ser His Trp Leu Val Tyr Ala Asn Ser
 819 828 837
 GCC GCC AAT CCC CTC CTC TAC TCC TTC CTC CCT 3'

 Ala Ala

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FIGURE 74



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FIGURE 75

10 μ M ATP

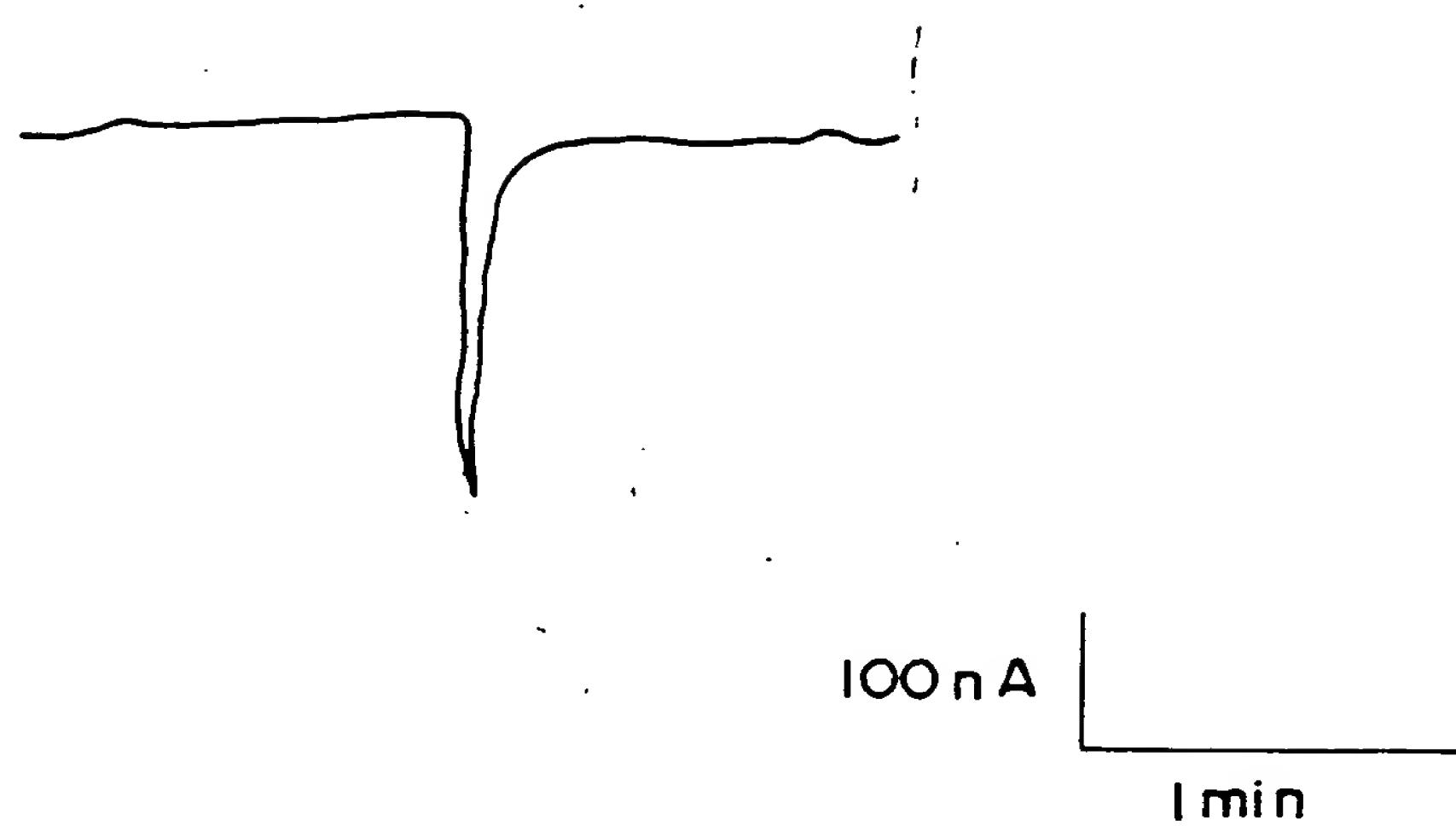


FIGURE 76

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h3H2-17 (5-3)	10	1	10	20	30	40	50	50
p3H2-17 (5')			1	GTGGCCCTGG	TGGCAACAT	CCTGGCTTC	TGGCACAGC	GTGGAGGTGG
h3H2-17 (5-3)	60	51	60	70	80	90	100	100
p3H2-17 (5')		51	CCGTCTCT	TGGTAGTGT	GTGGAGTCGT	GTGGCTGGCT	GTGGAGCGG	GTGGAGCGG
h3H2-17 (5-3)	110	101	110	120	130	140	150	150
p3H2-17 (5')		101	ACGTCTCC	GTGGCCATC	TTCCTCTCA	CACCCATCA	GGTAAACCC	GGTAAACCC
h3H2-17 (5-3)	160	151	160	170	180	190	200	200
p3H2-17 (5')		151	ACTTCCT	ATGACCTAC	CCGGCTGGC	CTGGCCACC	ATGATATGCC	ATGATATGCC
h3H2-17 (5-3)	210	201	210	220	230	240	250	250
p3H2-17 (5')		201	CTAACCTAC	GTGGCTGG	TCACTCTCA	CCCTCTCC	TTGCTGGC	TTGCTGGC
h3H2-17 (5-3)	260	251	260	270	280	290	300	300
p3H2-17 (5')		251	TCCTGGCT	CTACCTCT	CTGGCTGG	CTGGCTGG	CTGCTGG	CTGCTGG
h3H2-17 (5-3)	310	301	310	320	330	340	350	350
p3H2-17 (5')		301	CCAGCAGGTC	CTGGGGCCA	AGAGGGGGC	ACCAAGGGGG	CTCGTATGGC	CTCGTATGGC
h3H2-17 (5-3)	360	351	360	370	380	390	400	400
p3H2-17 (5')		351	TGTGGCTG	GCAGCTGCT	TGGCCCTCTG	TGGCTGCT	CTCTAC...	CTCTAC...

FIGURE 77

1	TGACTCCCTGAACATAGGAAACCCACCTGGCAGCCATGGAATGGGACAATGGCACAGGC	60
1	MetGluTrpAspAsnGlyThrGly	8
61	CAGGCTCTGGGCTTGCCACCCACCACCTGTGTCTACCGGGAGAGAACTTCAGCAACTGCTG	120
8	GlnAlaLeuGlyLeuProProThrThrCysValTyrArgGluAsnPheLysGlnLeuLeu	28
121	CTGCCACCTGTGTATTGGGGTGTGGCGGTGGCCCTGCCCTGCCGTGAAACATCTGTGTCA	180
28	LeuProProValTyrSerAlaValLeuAlaAlaGlyLeuProLeuAsnIleCysValIle	48
181	ACCCAGATCTGCACGTCCGCCGGCCCTGACCCGCACGGCCGTGTACACCCCTAAACCTT	240
48	ThrGlnIleCysThrSerArgArgAlaLeuThrArgThrAlaValTyrThrLeuAsnLeu	68
241	GCTCTGGCTGACCTGCTATATGCCCTGCTCCCTGCCCTGCTCATCTACAACATGCCAA	300
68	AlaLeuAlaAspLeuLeuTyrAlaCysSerLeuProLeuLeuIleTyrAsnTyrAlaGln	88
301	GGTGATCACTGGCCCTTGGCGACTTCGCCTGCCCTGGTCCGCTTCTCTTATGCC	360
88	GlyAspHisTrpProPheGlyAspPheAlaCysArgLeuValArgPheLeuPheTyrAla	108
361	AACCTGCACGGCAGCATTCTCTCACCTGCATCAGCTTCCAGCGCTACCTGGGCATC	420
108	AsnLeuHisGlySerIleLeuPheLeuThrCysIleSerPheGlnArgTyrLeuGlyIle	128
421	TGCCACCCGCTGGCCCCCTGGCACAAACGTGGGGCCGGCTGCCCTGGCTAGTGTGT	480
128	CysHisProLeuAlaProTrpHisLysArgGlyGlyArgArgAlaAlaTrpLeuValCys	148
481	GTAACCGTGTGGCTGGCCGTGACAACCCAGTGCCTGCCACAGCCATCTCGCTGCCACA	540
148	ValThrValTrpLeuAlaValThrThrGlnCysLeuProThrAlaIlePheAlaAlaThr	168
541	GGCATCCAGCGTAACCGCACTGTCTGCTATGACCTAGCCCGCTGCCCTGGCCACCCAC	600
168	GlyIleGlnArgAsnArgThrValCysTyrAspLeuSerProProAlaLeuAlaThrHis	188
601	TATATGCCCTATGGCATGGCTCTCACTGTCACTGGCTTCCCTGCTGCCCTTGCTGCCCTG	660
188	TyrMetProTyrGlyMetAlaLeuThrValIleGlyPheLeuLeuProPheAlaAlaLeu	208
661	CTGGCCTGCTACTGTCTCTGGCTGCCCTGCCCTGTGCCGCCAGGATGGCCCGGAGAGCCT	720
208	LeuAlaCysTyrCysLeuLeuAlaCysArgLeuCysArgGlnAspGlyProAlaGluPro	228
721	GTGGCCCAGGAGCGGGGTGGCAAGGCGGCCGGCATGGCGTGGTGGCTGCTGCCCTT	780
228	ValAlaGlnGluArgArgGlyLysAlaAlaArgMetAlaValValAlaAlaAlaPhe	248
781	GCCATCAGCTTGCCTTTCACATCACCAAGACAGCCTACCTGGCAGTGGCTCGACG	840
248	AlaIleSerPheLeuProPheHisIleThrLysThrAlaTyrLeuAlaValGlySerThr	268
841	CCGGCGTCCCCCTGCACTGTATTGGAGGCCTTGCAGCGGCCACAAAGGCACGCCCG	900
268	ProGlyValProCysThrValLeuGluAlaPheAlaAlaTyrLysGlyThrArgPro	288
901	TTTGCCAGTGCCAACAGCGTGCTGGACCCCACCTCTTACTTCACCCAGAAGAAGTTC	960
288	PheAlaSerAlaAsnSerValLeuAspProIleLeuPheTyrPheThrGlnLysPhe	308
961	CGCCGGCGACCACATGAGCTCTACAGAAACTCACAGCCAAATGGCAGAGGCAGGGTCGC	1020
308	ArgArgArgProHisGluLeuLeuGlnLysLeuThrAlaLysTrpGlnArgGlnGlyArg	328
1021	TGA	1023
328	***	329

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FIGURE 78

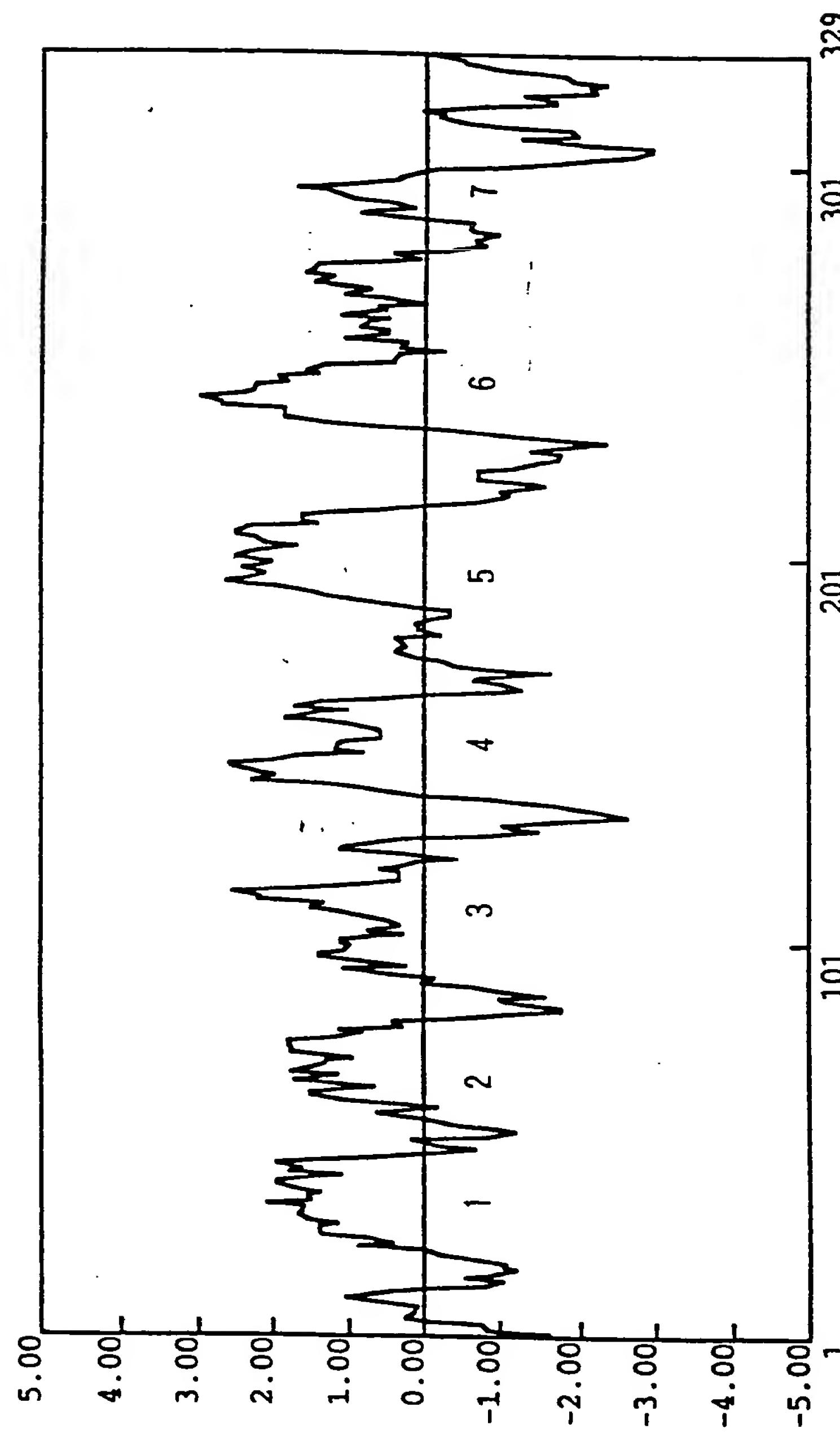


FIGURE 79

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human prino, mouseFULL3H2	1	MEWDNGTSAQ	10	LGLPPTTCVY	20	RENFKQLLLP	30	PVYSAVLAAG	40	EPNIVCIVIQ	50
	1	YEQDNGTIIQA		PGLPPTTCVY		REDFEKRLLLR		PVYSVMLWVG		EPNIVCIVIQ	50
human prino, mouseFULL3H2	51	ICtSRAALTR	60	TAVYTLNLAL	70	ADLYACSLP	80	LIIXNYAQGP	90	HMPFGDFACR	100
	51	ICASRRFLTR		SAVYTLNLAL		ADLYACSLP		LIIXNYAQRGD		HMPFGDFACR	100
human prino, mouseFULL3H2	101	LVRFLFYANL	110	HGSILFLTCI	120	PLAPNMHKRGCG	130	RRAAVLVCVT	140	150	
	101	FVRFLFYANL		HGSILFLTCI		PLASNMHKRGCG		RRAAVLVCVT		150	
human prino, mouseFULL3H2	151	VWLAVTQCL	160	ETAIFFAATGI	170	QRNRTVCYDI	180	SPPAIAATHYM	190	200	
	151	VWLAVTQCL		ETAVFFAATGI		QRNRTVCYDI		SPPILSTYI		200	
human prino, mouseFULL3H2	201	FLLPFAALLA	210	CYCLFCRLC	220	RQDGPAEPVA	230	PYGMALTVIG	240	250	
	201	FLLPFAALLA		CYCRMARRLC		RQDGPAEPVA		PYGMALTVIG		250	
human prino, mouseFULL3H2	251	SFLPFHITKT	260	AYLAVESTPG	270	VPCIVLEAFA	280	AAYKGTRPFA	290	300	
	251	SFLPFHITKT		AYLAVESTPG		VSQPYLEFA		AAYKGTRPFA		300	
human prino, mouseFULL3H2	301	FYFTCKRFR	310	RPHELLOQKLT	320	AKWQRQGR*	330	340	350	350	
	301	FYFTCKRFR		QPHDLQRLT		AKWQRQGR*			350	